



NAME/KEY: CDS  
LOCATION: (25) ... (372)  
US-10-178-449A-48

Query Match 47.0%; Score 209.4; DB 15; Length 529;  
Best Local Similarity 82.5%; Pred. No. 4.2e-48;  
Matches 24; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214  
DB 78 AGAATCTCGAGTGTGAGAGAGAGCTATGCGAAGAGCTAGCAAGACATGTCAGGCAA 137  
QY 215 CTGTGGCAATACGGGACATTTGACCAACATGTAATCATGGAGGGTGGCCCATGG 274  
DB 138 CTGTGGCAACACAGACATTTGTATATCAAGTGTCAATGGAGGGTGGCCCATGG 197  
QY 275 AGCGTGCATGTGGCTGAACGGGAAACATGTGTTCTGTTACTTCAATTGTAAAAAAGC 334  
DB 198 AGCTGTGCATGTGGCTGAGAGGAAACATGTGTTCTGTTACTTCAATTGTAAAAAAGC 257  
QY 335 CGAAAGCTTGCTCAAGACAACTTAAAGCCGAACTGCGCTCAAGACAACTTAATGC 394  
DB 258 TGAAGAACTCGCTCAAGATTAAGTAAAGACAGAGAGCTGCTAAAGACAACTCAAGGC 317  
QY 395 CGAAAGCTTGACCGGTGATGCCAAGAAAGTGTCCAAAGCTTGAACATCC 445  
DB 318 AGATAGTTTGACCATGATGCAAAAGATGATCAAAATGTGCAACATCC 368

## RESULT 2

US-10-178-449A-31  
Sequence 31, Application US/10178449A  
Publication No. US20030140368A1  
GENERAL INFORMATION:  
APPLICANT: Famodu, Omolayo O.  
APPLICANT: Herrmann, Rafael  
APPLICANT: Lu, Albert L.  
APPLICANT: McCutchen, Billy Fred  
APPLICANT: Miao, Guo-Hua  
APPLICANT: Presnail, James K.  
APPLICANT: Rafaleki, Jan Antoni  
APPLICANT: Weng, Zude  
TITLE OF INVENTION: Plant Defensins  
FILE REFERENCE: 35718/249123  
CURRENT APPLICATION NUMBER: US/10/178, 449A  
PRIOR FILING DATE: 2002-06-21  
PRIOR APPLICATION NUMBER: US 10/030,516  
PRIOR FILING DATE: 2000-05-03  
PRIOR APPLICATION NUMBER: PCT/US00/11952  
PRIOR FILING DATE: 2000-05-03  
PRIOR APPLICATION NUMBER: US 60/133,039  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 31  
LENGTH: 579  
TYPE: DNA  
ORGANISM: Vernonia mespilifolia  
US-10-178-449A-31

Query Match 45.5%; Score 203; DB 15; Length 579;  
Best Local Similarity 81.1%; Pred. No. 2.7e-46;  
Matches 236; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214  
DB 92 AGAATCTCGAGTGTGAGAGAGAGCTATGCGAAGAGCTAGCAAGACATGTCAGGCAA 151  
QY 215 CTGTGGCAATACGGGACATTTGACCAACATGTAATCATGGAGGGTGGCCCATGG 274  
DB 152 CTGTGGCAACACAGACATTTGTATATCAAGTGTAAAGCTAGGAGGGTGGCCCATGG 211  
QY 275 AGCGTGCATGTGGCTGAACGGGAAACATGTGTTCTGTTACTTCAATTGTAAAAAAGC 334

DB 212 AGCTGTGCATGTGCGGAGGAAACATGTCTTTTGTATTTCAATTGTAAAAAAGC 271  
QY 335 CGAAAGCTTGCTCAAGACAACTTAAAGCCGAAACATGCTCAAGACAACTTAATGC 394  
DB 272 TGAAGAACTCGCTCAAGATTAAGTTAAAGCTGAAGAGCTTGCAAAAGACAACTCAAGGC 331  
QY 395 CGAAAGCTTGACCGGTGATGCCAAGAAAGTGTTCGAACGTTGAACATCC 445  
DB 332 AGATAGTTTGACCATGATGCAAAAGATGATCAAAATGTGCAACATCC 382

## RESULT 3

US-10-178-449A-3  
Sequence 3, Application US/10178449A  
Publication No. US20030140368A1  
GENERAL INFORMATION:  
APPLICANT: Famodu, Omolayo O.  
APPLICANT: Herrmann, Rafael  
APPLICANT: Lu, Albert L.  
APPLICANT: McCutchen, Billy Fred  
APPLICANT: Miao, Guo-Hua  
APPLICANT: Presnail, James K.  
APPLICANT: Rafaleki, Jan Antoni  
APPLICANT: Weng, Zude  
TITLE OF INVENTION: Plant Defensins  
FILE REFERENCE: 35718/249123  
CURRENT APPLICATION NUMBER: US/10/178, 449A  
PRIOR FILING DATE: 2002-06-21  
PRIOR APPLICATION NUMBER: US 10/030,516  
PRIOR FILING DATE: 2000-05-03  
PRIOR APPLICATION NUMBER: PCT/US00/11952  
PRIOR FILING DATE: 2000-05-03  
PRIOR APPLICATION NUMBER: US 60/133,039  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 460  
TYPE: DNA  
ORGANISM: Dimorphotheca sinuata  
US-10-178-449A-3

Query Match 37.8%; Score 168.6; DB 15; Length 460;  
Best Local Similarity 81.6%; Pred. No. 1e-36;  
Matches 195; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214  
DB 87 AGAATCGGACCTGTGAGAAAGTGTGAGAAAGCTAGCAAGACATGTCAGGCAA 146  
QY 215 CTGTGGCAATACGGGACATTTGACCAACATGTAATCATGGAGGGTGGCCCATGG 274  
DB 147 CTGTGGCAACAGGAGACATGTGACAGACAGTAAAGTGTGGAGACATGACCCATGG 206  
QY 275 AGCGTGCATGTGGCTGAACGGGAAACATGTGTTCTGTTACTTCAATTGTAAAAAAGC 334  
DB 207 TGGGTGTGCATGTGGCTGAGGAGGAAACATGTGTTCTGTTACTTCAATTGTAAAAAAGC 266  
QY 335 CGAAAGCTTGCTCAAGACAACTTAAAGCCGAAACATGCTCAAGACAACTTAATG 393  
DB 267 CGAAAGCTTGCCCAAGACAAAGCTTCAAGCTGTAATAATTCGCGGTGATGACGTTAAG 325

## RESULT 4

US-10-178-449A-1  
Sequence 1, Application US/10178449A  
Publication No. US20030140368A1  
GENERAL INFORMATION:  
APPLICANT: Famodu, Omolayo O.  
APPLICANT: Herrmann, Rafael  
APPLICANT: Lu, Albert L.  
APPLICANT: McCutchen, Billy Fred



```
Db      91 AGAAATCGATCGGTGAAGGAGAACTATGTGAGAGGCAAGCAATGCTTGAAGA 150
Qy      215 CTGTGGCAATACGGGACATTTGTGCAACCAATGTAAATCATGAGGGGTGCGCCCATGG 274
Db      151 TTGTGTAAACAACAAGACATTTGTGACGACCAATGCAAGCTTGGAGGGGTGACGCCATGG 210
Qy      275 AGCGTGTCAATGTGGGTAAACGGGAAACACATGTCTTTCTGTACTTCAATTGTAAAAAGC 334
Db      211 AGCTTGTCAATGTGGCGGTGGGAAACATGTGCTTCTGTACTTCCAGTGCCCAAGC 270
Qy      335 CGAAAGCTTGTCTCAAGCAAACTTAAGCCGAAACAATGCTGCTCAAGCAAACTTAATGC 394
Db      271 CGAGAAATGCGCCAGATTAACCTCCAGCTGAAGAGCTTGCACAGAGAAATTTGAAGC 330
Qy      395 CCAAAA 400
Db      331 TGAAGA 336
```

```
RESULT 7
US-10-178-449A-9
; Sequence 9, Application US/10178449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Presnail, James K.
; APPLICANT: Rafalski, Jan Antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Parthenium argentatum Grey
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 413
; OTHER INFORMATION: n = A,T,C or G
US-10-178-449A-9
```

```
Query Match      35.1%; Score 156.4; DB 15; Length 463;
Best Local Similarity 77.2%; Pred. No. 2.7e-33;
Matches 190; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy      155 AGATATCGATCCGTTAGTGAAGTATGAGAGAACTGACAAAGCATGTGCGGAAA 214
Db      94 AGAAATCGATCGGTGAAGGAGAACTATGTGAGAGGCAAGCAATGCTTGAAGA 153
Qy      215 CTGTGGCAATACGGGACATTTGTGCAACCAATGTAAATCATGAGGGGTGCGCCCATGG 274
Db      154 TTGTGTAAACAACAAGACATTTGTGACGACCAATGCAAGCTTGGAGGGGTGACGCCATGG 213
Qy      275 AGCGTGTCAATGTGGGTAAACGGGAAACACATGTCTTTCTGTACTTCAATTGTAAAAAGC 334
Db      211 AGCTTGTCAATGTGGCGGTGGGAAACATGTGCTTCTGTACTTCCAGTGCCCAAGC 273
Qy      335 CGAAAGCTTGTCTCAAGCAAACTTAAGCCGAAACAATGCTGCTCAAGCAAACTTAATGC 394
```

```
Db      274 CGAGAAATGCGCCAGATTAACCTCCAGCTGAAGAGCTTGCACAGAGAAATTTGAAGC 333
Qy      395 CCAAAA 400
Db      334 TGAAGA 339
```

```
RESULT 8
US-10-178-449A-11
; Sequence 11, Application US/10178449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Presnail, James K.
; APPLICANT: Rafalski, Jan Antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Parthenium argentatum Grey
US-10-178-449A-11
```

```
Query Match      35.1%; Score 156.4; DB 15; Length 603;
Best Local Similarity 77.2%; Pred. No. 3e-33;
Matches 190; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy      155 AGATATCGATCCGTTAGTGAAGTATGAGAGAACTGACAAAGCATGTGCGGAAA 214
Db      101 AGAAATCGATCGGTGAAGGAGAACTATGTGAGAGGCAAGCAATGCTTGAAGA 160
Qy      215 CTGTGGCAATACGGGACATTTGTGCAACCAATGTAAATCATGAGGGGTGCGCCCATGG 274
Db      161 TTGTGTAAACAACAAGACATTTGTGACGACCAATGCAAGCTTGGAGGGGTGACGCCATGG 220
Qy      275 AGCGTGTCAATGTGGGTAAACGGGAAACACATGTCTTTCTGTACTTCAATTGTAAAAAGC 334
Db      221 AGCTTGTCAATGTGGCGGTGGGAAACATGTGCTTCTGTACTTCCAGTGCCCAAGC 280
Qy      335 CGAAAGCTTGTCTCAAGCAAACTTAAGCCGAAACAATGCTGCTCAAGCAAACTTAATGC 394
Db      281 CGAGAAATGCGCCAGATTAACCTCCAGCTGAAGAGCTTGCACAGAGAAATTTGAAGC 340
Qy      395 CCAAAA 400
Db      341 TGAAGA 346

RESULT 9
US-10-178-449A-21
; Sequence 21, Application US/10178449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua
```

```
APPLICANT: Presnail, James K.
APPLICANT: Rafaleki, Jan antoni
APPLICANT: Meng, Zude
FILE OF INVENTION: Plant Defensins
FILE REFERENCE: 35718/249123
CURRENT APPLICATION NUMBER: US/10/178,449A
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 10/030,516
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: PCT/US00/11952
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 60/133,039
PRIOR FILING DATE: 1999-05-07
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 458
TYPE: DNA
ORGANISM: Parthenium argentatum Grey
FEATURE:
NAME/KEY: misc_feature
LOCATION: 322..375, 402..452
OTHER INFORMATION: n = A,T,C or G
US-10-178-449A-21
```

```
Query Match          34.7%; Score 154.8; DB 15; Length 458;
Best Local Similarity 76.8%; Pred. No. 7.4e-33;
Matches 189; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
```

```
QY 155 AGATATGCATCCGTTGATGAGAACTATGCGAAGAACTGACAAACATGTCGGGAAA 214
DB 72 AGAAATCGATCGGTGAGAGGAGAACTATGTGAGAAAGCAAGCAATGCTCGGAAA 131
QY 215 CTGTGCAATACGGGACATTTGTGCAACCAATGTAATCATGGAGGGTGGGCCCATGG 274
DB 132 TTGTGTACACACAGACAGACATGTGACGACCAATGCAAGCTTGGAGGGTGCAGCCATGG 191
QY 275 AGCGTGCATGTGCGTAACGGGAAACACATGTGTTCTGTTACTTCAATTGTAAGAAAGC 334
DB 192 AGCTGTGATGTGCGCGGTGGGAAACACATGTCTTCTGCTACTTCCAGTCCCAAGC 251
QY 335 CGAAAGCTTGCTCAGACAACTTAAGCCGAAACAATCGCTGCTAAGACAACTTAATGC 394
DB 252 CGAGAAATGAGCCCAAGATTAATCTCCGAGCTGAGAGAGCTTCCCAAGGAAAGATTGAAGC 311
QY 395 CCAAAA 400
DB 312 TGA AAA 317
```

```
RESULT 10
US-10-178-449A-17
Sequence 17, Application US/10178449A
Publication No. US20030140368A1
GENERAL INFORMATION:
APPLICANT: Farnodu, Omolayo O.
APPLICANT: Herrmann, Rafael
APPLICANT: Lu, Albert L.
APPLICANT: McCutchen, Billy Fred
APPLICANT: Miao, Guo-Hua
APPLICANT: Presnail, James K.
APPLICANT: Rafaleki, Jan antoni
APPLICANT: Meng, Zude
TITLE OF INVENTION: Plant Defensins
FILE REFERENCE: 35718/249123
CURRENT APPLICATION NUMBER: US/10/178,449A
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 10/030,516
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: PCT/US00/11952
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 60/133,039
PRIOR FILING DATE: 1999-05-07
```

```
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 460
TYPE: DNA
ORGANISM: Parthenium argentatum Grey
FEATURE:
NAME/KEY: misc_feature
LOCATION: 342
OTHER INFORMATION: n = A,T,C or G
US-10-178-449A-17
```

```
Query Match          34.7%; Score 154.8; DB 15; Length 460;
Best Local Similarity 76.8%; Pred. No. 7.4e-33;
Matches 189; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
```

```
QY 155 AGATATGCATCCGTTGATGAGAACTATGCGAAGAACTGACAAACATGTCGGGAAA 214
DB 89 AGAAATCGATCGGTGAGAGGAGAACTATGTGAGAAAGCAAGCAATGCTCGGAAA 148
QY 215 CTGTGCAATACGGGACATTTGTGCAACCAATGTAATCATGGAGGGTGGGCCCATGG 274
DB 149 TTGTGTACACACAGACAGACATGTGACGACCAATGCAAGCTTGGAGGGTGCAGCCATGG 208
QY 275 AGCGTGCATGTGCGTAACGGGAAACACATGTGTTCTGTTACTTCAATTGTAAGAAAGC 334
DB 209 AGCTGTGATGTGCGCGGTGGGAAACACATGTCTTCTGCTACTTCCAGTCCCAAGC 268
QY 335 CGAAAGCTTGCTCAGACAACTTAAGCCGAAACAATCGCTGCTAAGACAACTTAATGC 394
DB 269 CGAGAAATGAGCCCAAGATTAATCTCCGAGCTGAGAGAGCTTCCCAAGGAAAGATTGAAGC 328
QY 395 CCAAAA 400
DB 329 TGA AAA 334
```

```
RESULT 11
US-10-636-396-6
Sequence 6, Application US/10636396
Publication No. US20040073971A1
GENERAL INFORMATION:
APPLICANT: Bidney, Dennis L.
APPLICANT: Crasta, Oswald R.
APPLICANT: Duvick, Jon
APPLICANT: Hu, Xu
APPLICANT: Lu, Guhua
TITLE OF INVENTION: Sunflower Anti-Pathogenic Proteins and
FILE REFERENCE: 5718-90
CURRENT APPLICATION NUMBER: US/10/636,396
CURRENT FILING DATE: 2003-08-07
PRIOR APPLICATION NUMBER: US/09/589,733C
PRIOR FILING DATE: 2000-06-08
PRIOR APPLICATION NUMBER: 60/140,646
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/162,904
PRIOR FILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 565
TYPE: DNA
ORGANISM: Helianthus annuus
US-10-636-396-6
```

```
Query Match          34.6%; Score 154.2; DB 17; Length 565;
Best Local Similarity 76.5%; Pred. No. 1.2e-32;
Matches 189; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
```

```
QY 155 AGATATGCATCCGTTGATGAGAACTATGCGAAGAACTGACAAACATGTCGGGAAA 214
DB 99 AGAAATCGATCGGTGAGAGGAGAACTATGTGAGAAAGCAAGCAATGCTCGGAAAC 158
```

Oy		215	CTGTGGCAATACGGGACATTGTGAACAACCAATTAATCATGGAGGGTGCAGCCCATGG	274
Db		159	ATGTGGCAAGCAAACACTGTGATGACCAAGTGCAAGTTTGGAGGGTGCAGCCCATGG	218
Oy		275	AGCGTGTATGTGCGCTTAACGGGAAACACATGTGTCTTCTGTAACCTTCATTTGAAAAAGC	334
Db		219	AGCTGTACACGCCCGCCGATGGGAAAACACATGTGCTTCTGTCATCTTCACTGTTCCAAAGC	278
Oy		335	CGAAAAGCTGTGTCAAAGCAAACTTAAGCGGACAACTCGCTCAAGACAAACCTTAATGCG	394
Db		279	CCAGAGTTGGCTTCAGATTAACCTCAGAGCGGAGAGAGCTCGCCAGAGAAATTGAACC	338
Oy		395	CCAAAAG 401 	
Db		339	CGAAAAG 345	

RESULT 12

US-10-636-026-6

Sequence 6, Application US/10636026

Publication No. US20040111761A1

GENERAL INFORMATION:

APPLICANT: Bidney, Dennis L.

APPLICANT: Craete, Oswald R.

APPLICANT: Huvi, Jon

APPLICANT: Hu, Xu

APPLICANT: Lu, Guihua

TITLE OF INVENTION: Sunflower Anti-pathogenic Proteins and

TITLE OF INVENTION: Genes and Their Uses

FILE REFERENCE: 5718-90

CURRENT APPLICATION NUMBER: US/10/636,026

CURRENT FILING DATE: 2003-08-07

PRIOR APPLICATION NUMBER: US/09/589,733C

PRIOR FILING DATE: 2000-06-08

PRIOR APPLICATION NUMBER: 60/140,646

PRIOR FILING DATE: 1999-06-23

PRIOR APPLICATION NUMBER: 60/162,904

PRIOR FILING DATE: 1999-11-01

NUMBER OF SEQ ID NOS: 41

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 6

LENGTH: 565

TYPE: DNA

ORGANISM: Helianthus annuus

US-10-636-026-6

Query Match 34.6%; Score 154.2; DB 18; Length 565;

Best Local Similarity 76.5%; Pred. No. 1.2e-32;

Matches 189; Conservative 0; Mismatches 58; Indels 0; Gaps 0

Oy		155	AGATTGCGATCCGTTAGTGGAGAACTATGGAGAAAGCTACCAAGACATGSGTCGGGAAA	214
Db		99	AGAAATCGGATCGGTGAAGAGAAATTATGTAGAAAGGCAAGCACATGTGCGGAAC	158
Oy		215	CTGTGGCAATACGGGACATTGTGAACAACCAATTAATCATGGAGGGTGCAGCCCATGG	274
Db		159	ATGTGGCAAGCAAACACTGTGATGACCAAGTGCAAGTTTGGAGGGTGCAGCCCATGG	218
Oy		275	AGCGTGTATGTGCGCTTAACGGGAAACACATGTGTCTTCTGTAACCTTCATTTGAAAAAGC	334
Db		219	AGCTGTACACGCCCGCCGATGGGAAAACACATGTGCTTCTGTCATCTTCACTGTTCCAAAGC	278
Oy		335	CGAAAAGCTGTGTCAAAGCAAACTTAAGCGGACAACTCGCTCAAGACAAACCTTAATGCG	394
Db		279	CCAGAGTTGGCTTCAGATTAACCTCAGAGCGGAGAGAGCTCGCCAGAGAAATTGAACC	338
Oy		395	CCAAAAG 401 	
Db		339	CGAAAAG 345	

RESULT 13

```

US-10-178-449A-19
; Sequence 19, Application US/10178449A
; Publication No. US20030140368A1
GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Presnail, James K.
; APPLICANT: Rafaleki, Jan antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ. ID NOS: 51
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 464
; TYPE: DNA
; ORGANISM: Parthenium argentatum Grey
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 445..452
; OTHER INFORMATION: n = A,T,C or G
US-10-178-449A-19

Query Match          34.3%; Score 153.2; DB 15; Length 464;
Best Local Similarity 76.4%; Pred. No. 2,1e-32;
Matches 188; Conservative 0; Mismatches 58; Indels 0; Gaps 0

QY 155 AGATATCGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214
Db 94 AGAATCGGATCGGTGGAAGGAGAACTATGTGAAGAGCAAGACATGTCGGA 153

QY 215 CTGGGCAATACGGGACATGTGTGACCAACCAATGTAAATCATGGAGAGGTCGGCCCATGG 274
Db 154 TTGGGTGAACCAAGACACTGTGTGACCAACCAATGTGAAGTCTTGGAGGGGTGAGCCCATGG 213

QY 275 AGCGTGTATGTGCGTAAACGGGAACACATGTGTTCTGTACTTCAATTGTAAAAAGC 334
Db 214 AGCTTGTATGTGGCGCGGTGGAAACACATGTGCTTGTCTACTTCCAGTGCCCAAGC 273

QY 335 CGAAAAGCTTGCTCAAGCAAACTTAAAGCCGAAACCACTCGCTCAAGCAAACTTAATGC 394
Db 274 CGAAGATGAGCCAGGATTAACCTCGAGCTGAAGAGAGCTTCCAAAGGAAAGATTGAAGT 333

QY 395 CCAAAA 400
Db 334 TGAATA 339

RESULT 14
US-10-178-449A-23
; Sequence 23, Application US/10178449A
; Publication No. US20030140368A1
GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Presnail, James K.
; APPLICANT: Rafaleki, Jan antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins

```

```
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: ParesEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Parthenium argentatum Grey
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 368
; OTHER INFORMATION: n = A,T,C or G
US-10-178-449A-23
```

```
Query Match 34.3%; Score 153.2; DB 15; Length 472;
Best Local Similarity 76.4%; Pred. No. 2.1e-32;
Matches 188; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
```

```
QY 155 AGATATGCAATCCGTTAGTGAGAACTATGCGAAGAACTAGCAAGACATGTCGGGAAA 214
DB 86 AGAATCGATCGGTGAGAGGAGAACTATGAGAAAGCAAGACATGTCGAGAA 145
QY 215 CTGTGCAATACGGGACATTTGTGACAACTAATGTAATCATGGAGGGTGGCCCATGG 274
DB 146 TTGTGTTAACACAAAGACATGTCGACCAATGCAATGCAAGTCTGGAGGGTGGCCCATGG 205
QY 275 AGCGTGCATGTGCGTAAACGGGAAACATGTGTTCTGTACTTCAATGTATAAAGC 334
DB 206 AGCTTGCAATGTGCGCGGTGGGAAACATGTGCTTCTGCACTTCCAGTGCCCAAGC 265
QY 335 CGAAAGCTTGCTCAAGCAAACTTAAAGCCGAACTGCGCTCAAGCAAACTTAATGC 394
DB 266 CGAGAAATGCGCCAGATTAACCTCGAGCTGAAGAGCTTGCCAAAGAGAAATTGAAGT 325
QY 395 CCAAAA 400
DB 326 TGA AAA 331
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RESULT 15
US-10-178-449A-15
; Sequence 15, Application US/10/178,449A
; Publication No. US20030140368A1
; GENERAL INFORMATION:
; APPLICANT: Farnodu, Omolayo O.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert U.
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Presnall, James K.
; APPLICANT: Rafalski, Jan Antoni
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Defensins
; FILE REFERENCE: 35718/249123
; CURRENT APPLICATION NUMBER: US/10/178,449A
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 10/030,516
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/US00/11952
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 60/133,039
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: ParesEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 439
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; TYPE: DNA
; ORGANISM: Parthenium argentatum Grey
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 276, 288, 349, 438
; OTHER INFORMATION: n = A,T,C or G
US-10-178-449A-15
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Query Match 31.0%; Score 138.4; DB 15; Length 439;
Best Local Similarity 71.9%; Pred. No. 2.8e-28;
Matches 192; Conservative 0; Mismatches 74; Indels 1; Gaps 1;
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QY 155 AGATATGCAATCCGTTAGTGAGAACTATGCGAAGAACTAGCAAGACATGTCGGGAAA 214
DB 93 AGAATCGATCGGTGAGAGGAGAACTATGAGAAAGCAAGACATGTCGAGAAA 152
QY 215 CTGTGCAATACGGGACATTTGTGACAACTAATGTAATCATGGAGGGTGGCCCATGG 274
DB 153 TTGTGTTAACACAAAGACATTTGTGACCAATGCAAGTCTGGAGGGTGGCCCATGG 212
QY 275 AGCGTGCATGTGCGTAAACGGGAAACATGTGTTCTGTACTTCAATGTATAAAGC 334
DB 213 AGCTTGCAATGTGCGCGGTGGGAAACATGTGCTTCTGCACTTCCAGTGCCCAAGC 272
QY 335 CGAAAGCTTGCTCAAGCAAACTTAAAGCCGAACTGCTCAAGCAAACTTAATGC 393
DB 273 CGAAGATGCGCCAGATTAACCTCGAGCTGAAGAGCTTGCCAAAGAGAAATTGAA 332
QY 394 CCAAAAAGCTTGACCGTATGCCAAG 420
DB 333 GCTGAAAAAGAGCCAGCAAACTTGA 359
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Search completed: March 18, 2005, 19:33:33
Job time : 422 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 18, 2005, 06:45:35 ; Search time 388 Seconds  
(without alignment)  
6804.651 Million cell updates/sec

Title: US-09-763-019-5  
Perfect score: 446  
Sequence: 1 atggtcagtcgctgcgttc.....ttccaacgtgaacatcgcg 446

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	446	100.0	446	AA251379	AA251379 Dahlia me
2	446	100.0	446	AA299323	AA299323 DNA encod
3	287.2	64.4	606	AA299326	AA299326 DNA encod
4	284	63.7	557	AA299336	AA299336 DNA encod
5	215.2	48.3	534	AA251396	AA251396 Portion o
6	215.2	48.3	534	AA299325	AA299325 DNA encod
7	212	47.5	485	AA299335	AA299335 DNA encod
8	209.4	47.0	529	ADM77231	ADM77231 Ironweed
9	203	45.5	579	ADM77214	ADM77214 Dahlia me
10	177.2	39.7	577	AA251378	AA251378 Dahlia me
11	173.2	38.8	485	AA299333	AA299333 DNA encod
12	172.2	38.6	446	AA299329	AA299329 DNA encod
13	170	38.1	1093	AA299334	AA299334 DNA encod
14	169.2	37.9	522	AA299324	AA299324 DNA encod
15	168.6	37.8	460	AA254387	AA254387 Plant def
16	168.6	37.8	460	ADM77186	ADM77186 African d
17	168.6	37.8	503	AA254386	AA254386 Plant def
18	168.6	37.8	503	ADM77184	ADM77184 African d
19	167.2	37.5	534	AA299327	AA299327 DNA encod
20	166	37.2	434	AA299332	AA299332 DNA encod

21	166	37.2	437	3	AA299331	AA299331 DNA encod
22	166	37.2	443	3	AA299330	AA299330 DNA encod
23	166	37.2	488	3	AA299338	AA299338 DNA encod
24	166	37.2	575	3	AA299339	AA299339 DNA encod
25	165.6	37.1	316	3	AA251397	AA251397 Portion o
26	165.6	37.1	316	3	AA299328	AA299328 DNA of pF
27	164	36.8	485	3	AA299337	AA299337 DNA encod
28	161	36.1	461	11	ADM77229	ADM77229 Sunflower
29	157.8	35.4	523	3	AA251376	AA251376 Dahlia me
30	156.4	35.1	457	5	AA254392	AA254392 Plant def
31	156.4	35.1	457	11	ADM77186	ADM77186 Mexican r
32	156.4	35.1	463	5	AA254390	AA254390 Plant def
33	156.4	35.1	463	11	ADM77192	ADM77192 Mexican r
34	156.4	35.1	603	5	AA254391	AA254391 Plant def
35	156.4	35.1	603	11	ADM77194	ADM77194 Mexican r
36	154.8	34.7	458	5	AA254396	AA254396 Plant def
37	154.8	34.7	458	11	ADM77204	ADM77204 Mexican r
38	154.8	34.7	460	5	AA254394	AA254394 Plant def
39	154.8	34.7	460	11	ADM77200	ADM77200 Mexican r
40	154.2	34.6	565	5	AA254395	AA254395 Plant def
41	153.2	34.3	464	5	AA254395	AA254395 Plant def
42	153.2	34.3	464	11	ADM77202	ADM77202 Mexican r
43	153.2	34.3	472	5	AA254397	AA254397 Plant def
44	153.2	34.3	472	11	ADM77206	ADM77206 Mexican r
45	146.8	32.9	399	3	AA251375	AA251375 Dahlia me

## ALIGNMENTS

RESULT 1  
AA251379  
ID AA251379 standard; DNA; 446 BP.  
XX  
AC AA251379;  
XX  
DT 06-JUN-2000 (first entry)  
XX  
DE Dahlia merckii antimicrobial protein Dm-AMPI gene.  
XX  
KW Antimicrobial protein; Dm-AMPI; transgenic plant; microbial infection;  
KW bacteria; fungi; field crop; fruit; vegetable; canola; banana; sunflower;  
KW apple; ds.  
XX  
XX OS Dahlia merckii.  
XX  
FH Key Location/Qualifiers  
FT CDS  
FT /\*tag= a  
FT /product= "Antimicrobial protein Dm-AMPI"  
FT /note= "Does not include stop codon"  
FT /partial  
FT sig\_peptide  
FT 1..176  
FT /\*tag= e  
FT /note= "excludes intron"  
FT exon  
FT 1..64  
FT /\*tag= b  
FT /number= 1  
FT intron  
FT 65..156  
FT /\*tag= c  
FT /number= 1  
FT exon  
FT 157..446  
FT /\*tag= d  
FT /number= 2  
FT mat\_peptide  
FT 177..326  
FT /\*tag= f  
FT /product= "Mature Dm-AMPI protein"  
FT misc\_feature  
FT 327..446  
FT /\*tag= g  
FT /note= "Encodes protein which may be used as cleavable  
linker in the co-expression of multiple proteins"  
XX  
PN WO20001196-A1.



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Db      121 TTTATGTGTTCTGACAAAGTTGCAAAATATTGAGATGATCGATCCGTTAGTGAAGAC 180
Qy      181 TATGCGGAAGAGCTAGAGACATGTCGGGAAACCTGTGCAATAGCGGACATTGTGACA 240
Db      181 TATGCGGAAGAGCTAGAGACATGTCGGGAAACCTGTGCAATAGCGGACATTGTGACA 240
Qy      241 ACCAATTAATCATGAGAGGAGTGCAGCCCATGAGAGCGTGCATGTCGTAACCGGAAAC 300
Db      241 ACCAATTAATCATGAGAGGAGTGCAGCCCATGAGAGCGTGCATGTCGTAACCGGAAAC 300
Qy      301 ACATGTCCTTCTGTTACTTCAATTGTAAATAAGCCGAAAGCTTGCTCAAGACAACTTA 360
Db      301 ACATGTCCTTCTGTTACTTCAATTGTAAATAAGCCGAAAGCTTGCTCAAGACAACTTA 360
Qy      361 AAGCGGAACAACCTGCTCAAGACAACTTAATGCGCCAAAGCTTGACCGGTGATGCCAAGA 420
Db      361 AAGCGGAACAACCTGCTCAAGACAACTTAATGCGCCAAAGCTTGACCGGTGATGCCAAGA 420
Qy      421 AAGTGTTCCTCAACGTTGAACATCCG 446
Db      421 AAGTGTTCCTCAACGTTGAACATCCG 446

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RESULT 3  
AAZ99326  
ID AAZ99326 standard; DNA; 606 BP.

XX  
AC AAZ99326;  
XX  
DT 03-JUL-2000 (first entry)  
XX  
DE DNA encoding a fusion protein of DmAMP1 and RaAFP2.

XX  
KW Antimicrobial protein; AMP1; transgenic plant; linker propeptide;  
XX protein expression; plant defensin; RaAFP2; antifungal protein; AFP2; ss.  
XX  
OS Synthetic.  
XX Dahlia merckii.  
OS Undentified.

XX  
FH Key Location/Qualifiers  
FT CDS 76..597  
FT FT /\*tag= a  
FT FT 160..309  
FT FT /\*tag= b  
FT FT /note= "encodes DmAMP1"  
FT FT 442..594  
FT FT /\*tag= c  
FT FT /note= "encodes RaAFP2"

XX  
PN WO200011175-A1.

XX  
PD 02-MAR-2000.

XX  
PF 17-AUG-1999; 99WO-GB002716.

XX  
PR 18-AUG-1998; 98GB-00018001.

XX  
PR 04-DEC-1998; 98GB-00026753.

XX  
PA (ZENE ) ZENECA LTD.

XX  
PI Broekert WF, Francois IEUA, De Bolle MFC, Evans IJ, Ray JA;

XX  
DR WPI; 2000-246564/21.

XX  
DR P-PSDB; AAY84059.

XX  
PT Improving expression of polypeptides in plants involves coexpression of  
XX two or more proteins in plants within a single transcription unit.

XX  
PS Example 2; Fig 11; 15pp; English.

XX  
CC The present sequence encodes a protein of the invention, comprising the

CC mature proteins of the plant defensins, the Dahlia antimicrobial protein  
CC (AMP) 1 and the antifungal protein 2 (AFP2), linked by a linker  
CC propeptide of the invention. The specification describes methods for  
CC improving expression levels of one or more proteins in a transgenic  
CC plant. The method comprises inserting a DNA sequence having a promoter  
CC region operably linked to two or more protein encoding regions separated  
CC by a DNA sequence coding for a linker propeptide and a terminator region.  
CC The method is used to produce proteins in plants. The linker propeptide  
CC comprising a cleavage site, whereby the expressed polypeptide is post-  
CC translationally processed into the component protein molecules. The  
CC propeptide sequence is rich in amino acids A, V, S and T and contains  
CC dipeptide sequences consisting of either two acidic, two basic or one  
CC acidic and one basic residue as a cleavable linker sequence  
XX

SO Sequence 606 BP; 189 A; 136 C; 137 G; 144 T; 0 U; 0 Other;  
Query Match 64.4%; Score 287.2; DB 3; Length 606;  
Best Local Similarity 99.0%; Pred. No. 6.1e-69;  
Matches 289; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      155 AGATATGCAATCCGTTAGTGAAGAACTATGCGAAGAACTAGCAAGACATGTCGGGAAA 214
Db      138 AGATATGCAATCCGTTAGTGAAGAACTATGCGAAGAACTAGCAAGACATGTCGGGAAA 197
Qy      215 CTGTGGCAATACGAGACATTGTGACCAATGTAAATCATGAGAGGTCGCGCCATGG 274
Db      198 CTGTGGCAATACGAGACATTGTGACCAATGTAAATCATGAGAGGTCGCGCCATGG 257
Qy      275 AGCGTTCATGTCGCTTAACGGGAAACATGCTGTTTGTGTTACTTCAATTGTAAATAAGC 334
Db      258 AGCGTTCATGTCGCTTAACGGGAAACATGCTGTTTGTGTTACTTCAATTGTAAATAAGC 317
Qy      335 CGAAAGCTTGTCTCAAGACAACTTAAGCCGAAACATGCTGCTCAAGACAACTTAATGC 394
Db      318 CGAAAGCTTGTCTCAAGACAACTTAAGCCGAAACATGCTGCTCAAGACAACTTAATGC 377
Qy      395 CCAAAAGCTTGACCGGTGATGCCAAGAAAGTGTTCCAACGTTGAACATCCG 446
Db      378 CCAAAAGCTTGACCGGTGATGCCAAGAAAGTGTTCCAACGTTGAACATCCG 429

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RESULT 4  
AAZ99336  
ID AAZ99336 standard; DNA; 557 BP.

XX  
AC AAZ99336;

XX  
DT 03-JUL-2000 (first entry)

XX  
DE DNA encoding a fusion protein of DmAMP1 and RaAFP2.

XX  
KW Antimicrobial protein; AMP1; transgenic plant; linker propeptide;  
XX protein expression; plant defensin; RaAFP2; antifungal protein; AFP2; ss.

XX  
OS Synthetic.  
XX Dahlia merckii.  
OS Undentified.

XX  
FH Key Location/Qualifiers  
FT CDS 3..548  
FT FT /\*tag= a  
FT FT /product= "fusion protein of DmAMP1 and RaAFP2"

XX  
PN WO200011175-A1.

XX  
PD 02-MAR-2000.

XX  
PF 17-AUG-1999; 99WO-GB002716.

XX  
PR 18-AUG-1998; 98GB-00018001.

XX  
PR 04-DEC-1998; 98GB-00026753.

XX  
PA (ZENE ) ZENECA LTD.

XX PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;  
 XX WPI; 2000-246564/21.  
 DR P-PSDB; AAY64069.  
 XX  
 PT Improving expression of polypeptides in plants involves coexpression of  
 PT two or more proteins in plants within a single transcription unit.  
 XX  
 PS Disclosure; Fig 31; 151pp; English.  
 XX  
 CC The present sequence encodes a protein of the invention, comprising the  
 CC mature proteins of the plant defensins, the Dahlia antimicrobial protein  
 CC (AMP) 1 and the antifungal protein 2 (RAFP2), linked by a linker  
 CC propeptide of the invention. The specification describes methods for  
 CC improving expression levels of one or more proteins in a transgenic  
 CC plant. The method comprises inserting a DNA sequence having a promoter  
 CC region operably linked to two or more protein encoding regions separated  
 CC by a DNA sequence coding for a linker propeptide and a terminator region.  
 CC The method is used to produce proteins in plants. The linker propeptide  
 CC comprising a cleavage site, whereby the expressed polypeptide is post-  
 CC translationally processed into the component protein molecules. The  
 CC propeptide sequence is rich in amino acids A, V, S and T and contains  
 CC dipeptidic sequences consisting of either two acidic, two basic or one  
 CC acidic and one basic residue as a cleavable linker sequence  
 CC  
 XX Sequence 557 BP; 164 A; 122 C; 143 G; 128 T; 0 U; 0 Other;  
 SQ  
 Query Match 63.7%; Score 284; DB 3; Length 557;  
 Best Local Similarity 98.3%; Pred. No. 4,56-68;  
 Matches 287; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 155 AGATATCGATCCGTAGTGAAGAACTATGCGAAGAACTAGCAAGACATGTCGGGAAA 214  
 DB 65 AGATATCGATCCGTAGTGAAGAACTATGCGAAGAACTAGCAAGACATGTCGGGCAA 124  
 QY 215 CTGTGGCAATACGGGAACTTGTGCAACCAATGTAATTCATGGAGGTCGGCCCATGG 274  
 DB 125 CTGTGGCAATACGGGAACTTGTGCAACCAATGTAATTCATGGAGGTCGGCCCATGG 184  
 QY 275 AGCGTGCATGTGCGTAAACGGGAAACACATGTGTTCTGTACTTCAATTGTAAAAAAGC 334  
 DB 185 AGCGTGCATGTGCGTAAACGGGAAACACATGTGTTCTGTACTTCAATTGTAAAAAAGC 244  
 QY 335 CGAAAGCTTGCTCAGACAACTTAAAGCCGAAACATCGCTCAGACAACTTAAATGC 394  
 DB 245 CGAAAGCTTGCTCAGACAACTTAAAGCCGAAACATCGCTCAGACAACTTAAATGC 304  
 QY 395 CGAAAGCTTGACCGGTATGCCAAGAAAGTGTCCCAAGCTTGAATATCG 446  
 DB 305 CGAAAGCTTGACCGGTATGCCAAGAAAGTGTCCCAAGCTTGAATATCG 356  
 RESULT 5  
 AAZ51396  
 ID AAZ51396 standard; DNA; 534 BP.  
 XX  
 AC AAZ51396;  
 XX  
 DT 06-JUN-2000 (first entry)  
 XX  
 DE Portion of pFAJ106 encoding Dahlia merckii antimicrobial protein.  
 XX  
 KW Antimicrobial protein; DmAMP; transgenic plant; microbial infection;  
 KW bacteria; fungi; field crop; fruit; vegetable; canola; banana; sunflower;  
 KW apple; plant transformation vector; ds.  
 XX  
 OS Dahlia merckii.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 76..525  
 FT /\*tag= a

FT  
 XX  
 PN WO20001196-A1.  
 XX  
 PD 02-MAR-2000.  
 XX  
 PF 17-AUG-1999; 99WO-GB002720.  
 XX  
 PR 18-AUG-1998; 98GB-00018003.  
 XX  
 PA (ZENEC) ZENEC LTD.  
 XX  
 PI Evans IJ, Ray JA;  
 XX WPI; 2000-237658/20.  
 DR P-PSDB; AAY70323.  
 XX  
 PT Polynucleotide sequences and expression products useful for producing  
 PT transgenic plants that are resistant to microbial infections.  
 XX  
 PS Example 3; Fig 7; 77pp; English.  
 XX  
 CC The present sequence corresponds to the region between XhoI and SacI  
 CC sites of plant transformation vector pFAJ106, which encompass the coding  
 CC region for Dahlia merckii antimicrobial protein, Dm-AMP1. The vector is  
 CC useful in the production of transgenic plants which show improved  
 CC resistance to infections by microorganisms such as bacteria and fungi.  
 CC Transgenic plants include e.g. field crops, fruits and vegetables, such  
 CC as canola, sunflower, tomato, apple, banana, pear and mango  
 CC  
 XX Sequence 534 BP; 164 A; 118 C; 122 G; 130 T; 0 U; 0 Other;  
 SQ  
 Query Match 48.3%; Score 215.2; DB 3; Length 534;  
 Best Local Similarity 98.6%; Pred. No. 4e-49;  
 Matches 217; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 155 AGATATCGATCCGTAGTGAAGAACTATGCGAAGAACTAGCAAGACATGTCGGGAAA 214  
 DB 138 AGATATCGATCCGTAGTGAAGAACTATGCGAAGAACTAGCAAGACATGTCGGGCAA 197  
 QY 215 CTGTGGCAATACGGGAACTTGTGCAACCAATGTAATTCATGGAGGTCGGCCCATGG 274  
 DB 198 CTGTGGCAATACGGGAACTTGTGCAACCAATGTAATTCATGGAGGTCGGCCCATGG 257  
 QY 275 AGCGTGCATGTGCGTAAACGGGAAACACATGTGTTCTGTACTTCAATTGTAAAAAAGC 334  
 DB 258 AGCGTGCATGTGCGTAAACGGGAAACACATGTGTTCTGTACTTCAATTGTAAAAAAGC 317  
 QY 335 CGAAAGCTTGCTCAGACAACTTAAAGCCGAAACATC 374  
 DB 318 CGAAAGCTTGCTCAGACAACTTAAAGCCGAAACATC 357  
 RESULT 6  
 AAZ99325  
 ID AAZ99325 standard; DNA; 534 BP.  
 XX  
 AC AAZ99325;  
 XX  
 DT 03-JUL-2000 (first entry)  
 XX  
 DE DNA encoding a fusion protein of DmAMP1 and RAFP2.  
 XX  
 KW Antimicrobial protein; AMP1; transgenic plant; linker propeptide;  
 KW protein expression; plant defensin; RAFP2; antifungal protein; AFP2; ss.  
 XX  
 OS Synthetic.  
 OS Dahlia merckii.  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 76..522  
 FT /\*tag= a

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FT      misc_feature      160..309
FT      /*tag= b
FT      /note= "encodes DmAMP1"
FT      misc_feature      370..538
FT      /*tag= c
FT      /note= "encodes RsaFP2"
XX      WO200011175-A1.
XX      02-MAR-2000.
XX      17-AUG-1999; 99WO-GB002716.
XX      18-AUG-1998; 98GB-00018001.
XX      04-DEC-1998; 98GB-00026753.
XX      (ZENE ) ZENECA LTD.
XX      Broekaert WF, Francois IEJA, De Bolle MFC, Evans IU, Ray JA;
XX      WPI; 2000-246564/21.
XX      P-PSDB; AAY84058.
XX      Improving expression of polypeptides in plants involves coexpression of
XX      two or more proteins in plants within a single transcription unit.
XX      Example 2; Fig 9; 151pp; English.
XX      The present sequence encodes a protein of the invention, comprising the
XX      mature proteins of the plant defensins, the Dahlia antimicrobial protein
XX      (AMP) 1 and the antifungal protein 2 (AFP2), linked by a linker
XX      comprising a cleavage site, whereby the expressed polypeptide is post-
XX      translationally processed into the component protein molecules. The
XX      dipeptidic sequence is rich in amino acids A, V, S and T and contains
XX      acidic and one basic residue as a cleavable linker sequence
XX      Sequence 534 BP; 164 A; 118 C; 122 G; 130 T; 0 U; 0 Other;
XX      Query Match      48.3%; Score 215.2; DB 3; Length 534;
XX      Best Local Similarity 98.6%; Pred. No. 4e-49;
XX      Matches 217; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX      155 AGATATGCGATCCGTTAGTGGAGAACTATGCGAAGAACTAGCAAGCATGTGCGGAAA 214
XX      138 AGATATGCGATCCGTTAGTGGAGAACTATGCGAAGAACTAGCAAGCATGTGCGGAAA 197
XX      215 CTGTGGCAATACGGGACATTTGTGACAAACCAATGTAATCATGAGGGGTGCGCCCATGG 274
XX      198 CTGTGGCAATACGGGACATTTGTGACAAACCAATGTAATCATGAGGGGTGCGCCCATGG 257
XX      275 AGCGTGTCAATGTGGTAAACGGGAAACACATGTGTTCTGTTACTTCAATTTAAAAAAGC 334
XX      258 AGCGTGTCAATGTGGTAAACGGGAAACACATGTGTTCTGTTACTTCAATTTAAAAAAGC 317
XX      335 CGAAAAGCTTGCTCAAGCAAACTTTAAAGCCGAACAATCTC 374
XX      318 CGAAAAGCTTGCTCAAGCAAACTTTAAAGCCGAACAATCTC 357
XX      Db
XX      RESULT 7
XX      ID AA299335 standard; DNA; 485 BP.
XX      AC AA299335;
XX      DT 03-JUL-2000 (first entry)

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XX      DNA encoding a fusion protein of DmAMP1 and RsaFP2.
XX      DE Antimicrobial protein; AMP1; transgenic plant; linker polypeptide;
XX      KW protein expression; plant defensin; RsaFP2; antifungal protein; AFP2; ss.
XX      XX Synthetic.
XX      OS Dahlia merckii.
XX      OS Unidentified.
XX      FH Key
XX      FT CDS
XX      Location/Qualifiers
XX      FT      /*tag= a
XX      FT      /product= "fusion protein of DmAMP1 and RsaFP2"
XX      WO200011175-A1.
XX      02-MAR-2000.
XX      17-AUG-1999; 99WO-GB002716.
XX      18-AUG-1998; 98GB-00018001.
XX      04-DEC-1998; 98GB-00026753.
XX      (ZENE ) ZENECA LTD.
XX      Broekaert WF, Francois IEJA, De Bolle MFC, Evans IU, Ray JA;
XX      WPI; 2000-246564/21.
XX      P-PSDB; AAY84058.
XX      Improving expression of polypeptides in plants involves coexpression of
XX      two or more proteins in plants within a single transcription unit.
XX      Disclosure; Fig 30; 151pp; English.
XX      The present sequence encodes a protein of the invention, comprising the
XX      mature proteins of the plant defensins, the Dahlia antimicrobial protein
XX      (AMP) 1 and the antifungal protein 2 (RsaFP2), linked by a linker
XX      comprising a cleavage site, whereby the expressed polypeptide is post-
XX      translationally processed into the component protein molecules. The
XX      dipeptidic sequence is rich in amino acids A, V, S and T and contains
XX      acidic and one basic residue as a cleavable linker sequence
XX      Sequence 485 BP; 139 A; 104 C; 128 G; 114 T; 0 U; 0 Other;
XX      Query Match      47.5%; Score 212; DB 3; Length 485;
XX      Best Local Similarity 97.7%; Pred. No. 3e-48;
XX      Matches 215; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX      155 AGATATGCGATCCGTTAGTGGAGAACTATGCGAAGAACTAGCAAGCATGTGCGGAAA 214
XX      65 AGATATGCGATCCGTTAGTGGAGAACTATGCGAAGAACTAGCAAGCATGTGCGGAAA 124
XX      215 CTGTGGCAATACGGGACATTTGTGACAAACCAATGTAATCATGAGGGGTGCGCCCATGG 274
XX      125 CTGTGGCAATACGGGACATTTGTGACAAACCAATGTAATCATGAGGGGTGCGCCCATGG 184
XX      275 AGCGTGTCAATGTGGTAAACGGGAAACACATGTGTTCTGTTACTTCAATTTAAAAAAGC 334
XX      185 AGCGTGTCAATGTGGTAAACGGGAAACACATGTGTTCTGTTACTTCAATTTAAAAAAGC 244
XX      335 CGAAAAGCTTGCTCAAGCAAACTTTAAAGCCGAACAATCTC 374
XX      245 CGAAAAGCTTGCTCAAGCAAACTTTAAAGCCGAACAATCTC 284
XX      Db

```

RESULT 8  
ADM77231  
ID ADM77231 standard; cDNA; 529 BP.

AC ADM77231;

DT 03-JUN-2004 (first entry)

XX Ironweed cDNA encoding mature defensin #2.

XX Ironweed; ss; EST; expressed sequence tag; defensin;

XX soybean cyst nematode; pesticide; plant; plant pathogen;

XX Sclerotinia sclerotiorum; fungal infection; Candidiasis.

XX Vernonia mespilifolia.

XX US2003140368-A1.

XX 24-JUL-2003.

XX 21-JUN-2002; 2002US-00178449.

XX 25-OCT-2001; 2001US-00030516.

XX (PION-) PIONEER HI-BRED INT INC.

XX Famodu OO, Herrmann R, Lu AL, McCutchen BF, Miao G, Presnail JK;

XX Rafalski JA, Weng Z;

XX WPI; 2003-851760/79.

XX P-PSDB; ADM77232.

XX New nucleic acid molecule, useful for preparing a composition for

XX treating fungal infections, e.g. Candidiasis.

XX Claim 1; SEQ ID NO 48; 69pp; English.

XX The invention relates to an isolated nucleic acid molecule (either an

XX EST, expressed sequence tag or an EST contig) encoding a plant defensin

XX or its mature form, or the complement of them. Also included are a DNA

XX construct comprising the novel nucleic acid (operably linked to a

XX promoter that drives expression in a host cell), an expression cassette

XX comprising the DNA construct, a host cell having stably incorporated into

XX its genome the DNA construct, an isolated polypeptide and impacting a

XX plant pathogen e.g. soybean cyst nematode (Sclerotinia sclerotiorum). The

XX nucleic acid construct is useful for preparing a composition for treating

XX fungal infections, e.g. Candidiasis. The present sequence is either an

XX EST (expressed sequence tag) or an EST contig encoding a plant defensin

XX or its mature form.

XX Sequence 529 BP; 178 A; 88 C; 111 G; 148 T; 0 U; 4 Other;

XX Query Match 47.0%; Score 209.4; DB 11; Length 529;

XX Best Local Similarity 82.5%; Pred. No. 1.6e-47;

XX Matches 240; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

XX 155 AGATATCGATCCGTTAGTGAAGAACTATGCGAAGAACTAGCAAGACATGTCGGGAAA 214

XX 78 AGAAATCTGAGTGTGAGACAGAGCTATGCGAAGAACTAGCAAGACATGTCAGGCAA 137

QY 395 CCAAAAGCTTGACCGTGATGCCAAGAAAGTGGTTCCTCAAAAGCTTGAAACATCC 445

DB 318 AGATAAGTTTGACCATGATGCAAAAAGAGTAGTACCAATGTCGAACATCC 368

RESULT 9  
ADM77214  
ID ADM77214 standard; cDNA; 579 BP.

AC ADM77214;

DT 03-JUN-2004 (first entry)

XX Ironweed cDNA encoding mature defensin #1.

XX Ironweed; ss; EST; expressed sequence tag; defensin;

XX soybean cyst nematode; pesticide; plant; plant pathogen;

XX Sclerotinia sclerotiorum; fungal infection; Candidiasis.

XX Vernonia mespilifolia.

XX US2003140368-A1.

XX 24-JUL-2003.

XX 21-JUN-2002; 2002US-00178449.

XX 25-OCT-2001; 2001US-00030516.

XX (PION-) PIONEER HI-BRED INT INC.

XX Famodu OO, Herrmann R, Lu AL, McCutchen BF, Miao G, Presnail JK;

XX Rafalski JA, Weng Z;

XX WPI; 2003-851760/79.

XX P-PSDB; ADM77215.

XX New nucleic acid molecule, useful for preparing a composition for

XX treating fungal infections, e.g. Candidiasis.

XX Claim 1; SEQ ID NO 31; 69pp; English.

XX The invention relates to an isolated nucleic acid molecule (either an

XX EST, expressed sequence tag or an EST contig) encoding a plant defensin

XX or its mature form, or the complement of them. Also included are a DNA

XX construct comprising the novel nucleic acid (operably linked to a

XX promoter that drives expression in a host cell), an expression cassette

XX comprising the DNA construct, a host cell having stably incorporated into

XX its genome the DNA construct, an isolated polypeptide and impacting a

XX plant pathogen e.g. soybean cyst nematode (Sclerotinia sclerotiorum). The

XX nucleic acid construct is useful for preparing a composition for treating

XX fungal infections, e.g. Candidiasis. The present sequence is either an

XX EST (expressed sequence tag) or an EST contig encoding a plant defensin

XX or its mature form.

XX Sequence 579 BP; 198 A; 97 C; 117 G; 167 T; 0 U; 0 Other;

XX Query Match 45.5%; Score 203; DB 11; Length 579;

XX Best Local Similarity 81.1%; Pred. No. 9.5e-46;

XX Matches 236; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 155 AGATATCGATCCGTTAGTGAAGAACTATGCGAAGAACTAGCAAGACATGTCGGGAAA 214

DB 92 AGAAATCTGAGTGTGAGACAGAGCTATGCGAAGAACTAGCAAGACATGTCAGGCAA 151

QY 215 CTGTGGCAATACGGGAATTTGTGCAACCAATGTAATCATGGAGGGTGGCCCATGG 274

DB 138 CTGTGGCAACACAGGACATTTGTATATCATGTCAATGGAAGGTCAGCCCATGG 197

QY 275 AGCGTGCATGTGCGTAAACGGGAAACATGTGTTCTGTTAACTTCAATTTGTAAGG 334

DB 198 AGCTTGCATGTGCGTGAAGGAAACATGTGTTCTGTTAACTTCAATTTGTAAGG 257

QY 335 CGAAAAGCTTGCTCAAGACAACTTAAGCGGAACTGCGCTCAAGACAACTTAATGC 394

DB 258 TGAATAAAGCTGCTCAAGATTAAGCTTAAGAGGAAAGAGCTTGTAAAGACAACTCAAGGC 317

QY 335 CGAAAGCTTGCTCAAGACAACTTAAGCCGAACAACTGCTCAAGACAACTTAATGC 394  
 DB 272 TGAATAACTCGCTCAAGATTAAGTTAAAGCTGAAGACTTGCAAAAGACAACTCAAGGC 331  
 QY 395 CCAAAAGCTTGACCGTATGCGCAAGAAAGTGTTCCTCAAGCTTAACATCC 445  
 DB 332 AGATTAAGTTGACCATGATGCAAAAGAGTAGTACAAATGTGCAACATCC 382

## RESULT 10

AAZ51378  
 ID AAZ51378 standard; cDNA; 577 BP.  
 AC AAZ51378;  
 XX  
 XX

DT 06-JUN-2000 (first entry)  
 XX

DE Dahlia merckii antimicrobial protein Dm2.5 cDNA.  
 XX

KM Antimicrobial protein; DmAMP; Dm2.5; transgenic plant;  
 KM microbial infection; bacteria; fungi; field crop; fruit; vegetable;  
 KM canola; banana; sunflower; apple; ss.  
 XX

OS Dahlia merckii.  
 XX

Key Location/Qualifiers  
 FH 20..346  
 FT CDS  
 FT /\*tag= a  
 FT /product= "Antimicrobial protein Dm2.5"  
 FT /note= "Preprotein"  
 FT 20..103  
 FT sig\_peptide  
 FT /\*tag= b  
 FT 104..253  
 FT mat\_peptide  
 FT /\*tag= c  
 FT /product= "Mature Dm2.5 protein"  
 FT 254..343  
 FT /\*tag= d  
 FT /note= "Encodes protein which may be used as cleavable  
 linker in the co-expression of multiple proteins"  
 FT

PN W020001196-A1.  
 XX

PD 02-MAR-2000.  
 XX

PF 17-AUG-1999; 99WO-GB002720.  
 XX

PR 18-AUG-1998; 98GB-00018003.  
 XX

PA (ZENEC) ZENEC LTD.  
 XX

PI Evans LJ, Ray JA;  
 XX

XX WPI; 2000-237658/20.  
 XX

DR P-PSDB; AAY70314.  
 XX

PT Polynucleotide sequences and expression products useful for producing  
 transgenic plants that are resistant to microbial infections.  
 XX

PS Claim 1; Fig 3; 77pp; English.  
 XX

XX The present sequence is a Dahlia merckii cDNA encoding an antimicrobial  
 CC preprotein Dm2.5. This sequence is useful in the production of  
 CC transgenic plants which show improved resistance to infections by  
 CC microorganisms such as bacteria and fungi. Transgenic plants include e.g.  
 CC field crops, fruits and vegetables, such as canola, sunflower, tomato,  
 CC apple, banana, pear and mango  
 XX

SQ Sequence 577 BP; 178 A; 96 C; 140 G; 163 T; 0 U; 0 Other;  
 XX

Query March 39.7%; Score 177.2; DB 3; Length 577;  
 Best Local Similarity 80.1%; Pred. No. 1.2e-38;  
 Matches 234; Conservative 0; Mismatches 28; Indels 30; Gaps 1;

QY 155 AGATATCGATCCGTTAGTGAAGAACTATGCGAAGAACTAGACAGCATGTGCGGAAA 214  
 DB 82 AGATATCACAAGTGTGAGAGAAAGTATCGAAGAACTAGACAGCATGTGCGGAAA 141  
 QY 215 CTGTGGCAATAGCGGACATTTGTGACACCAATGAAATCATGGAGGTCGCGCCATGG 274  
 DB 142 CTGTGGCAACCGGACACTGTGACCAATGAAATCATGGAGGTCGCGCCATGG 201  
 QY 275 AGCGTGTATGTGCGTAAACGGAACACATGTGTTCTGTACTTCAATTTAAAAAGC 334  
 DB 202 GCGGTGCAAGTGTGAGAGGAAACACATGTGTTCTGTACTTCAAGTGTCCAAAGC 261  
 QY 335 CGAAAGCTTGCTCAAGACAACTTAAGCCGAACAACTGCTCAAGACAACTTAATGC 394  
 DB 262 CGAAAGCTT-----GCTCAAGACAAAGTTAATGC 291

## RESULT 11

AAZ99333  
 ID AAZ99333 standard; DNA; 485 BP.  
 XX  
 XX

AC AAZ99333;  
 XX

DT 03-JUL-2000 (first entry)  
 XX

DE DNA encoding a fusion protein of DmAMP1 and RsAFP2.  
 XX

KM Antimicrobial protein; AMP1; transgenic plant; linker propeptide;  
 KM protein expression; plant defensin; RsAFP2; antifungal protein; AFP2; ss.  
 XX

OS Synthetic.  
 OS Dahlia merckii.  
 OS unidentified.  
 XX

Key Location/Qualifiers  
 FH 3..476  
 FT CDS  
 FT /\*tag= a  
 FT /product= "fusion protein of DmAMP1 and RsAFP2"  
 FT

PN W020001175-A1.  
 XX

PD 02-MAR-2000.  
 XX

PF 17-AUG-1999; 99WO-GB002716.  
 XX

PR 18-AUG-1998; 98GB-00018001.  
 XX

PR 04-DEC-1998; 98GB-00026753.  
 XX

PA (ZENEC) ZENEC LTD.  
 XX

PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans LJ, Ray JA;  
 XX

XX WPI; 2000-246564/21.  
 XX

DR P-PSDB; AAY64066.  
 XX

PT Improving expression of polypeptides in plants involves coexpression of  
 two or more proteins in plants within a single transcription unit.  
 XX

PS Disclosure; Fig 28; 151pp; English.  
 XX

XX The present sequence encodes a protein of the invention, comprising the  
 CC mature proteins of the plant defensins, the Dahlia antimicrobial protein  
 CC (AMP) 1 and the antifungal protein 2 (AFP2), linked by a linker  
 CC propeptide of the invention. The specification describes methods for  
 CC improving expression levels of one or more proteins in a transgenic  
 CC plant. The method comprises inserting a DNA sequence having a promoter  
 CC region operably linked to two or more protein encoding regions separated  
 CC by a DNA sequence coding for a linker propeptide and a terminator region.  
 CC The method is used to produce proteins in plants. The linker propeptide

CC comprising a cleavage site, whereby the expressed polypeptide is post-  
CC translationally processed into the component protein molecules. The  
CC propeptide sequence is rich in amino acids A, V, S and T and contains  
CC dipeptidic sequences consisting of either two acidic, two basic or one  
CC acidic and one basic residue as a cleavable linker sequence  
XX

SO Sequence 485 BP; 124 A; 107 C; 128 G; 126 T; 0 U; 0 Other;

Query Match 38.8%; Score 173.2; DB 3; Length 485;

Best Local Similarity 85.1%; Pred. No. 1.5e-37;  
Matches 206; Conservative 0; Mismatches 33; Indels 3; Gaps 1;

155 AGATATGCGATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214

65 AGATATGCGATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 124

215 CTGTGGCAATACCGGACATTTGTGACCAACCAATGTAATCATGGAGGGTCCGCTCACGG 274

125 CTGTGGCAATACCGGACATTTGTGACCAACCAATGTAATCATGGAGGGTCCGCTCACGG 184

275 AGCGTGTATGTCGCTGTAACCGGAAACACATGTTTCTGTTACTTCAATTGTAATAAAGC 334

185 AGCGTGTATGTCGCTGTAACCGGAAACACATGTTTCTGTTACTTCAATTGTTGTAACGC 244

335 CGAAAGCTGCTCAAGACAACTTAAG---CCGACCACTGCTCAAGACAACTTA 391

245 TGAAGAAAGCTGCTGCTGCTTCTCTGTAAGCTTCTGTAAGAACTGCTCAAGAAAGCTCC 304

392 TG 393

305 TG 306

Db

RESULT 12

ID AA299329 standard; DNA; 446 BP.

AA299329;

03-JUL-2000 (first entry)

DNA encoding a fusion protein of DmAMP1 and RsaFP2.

Antimicrobial protein; AMP1; transgenic plant; linker propeptide;  
KW protein expression; plant defensin; RsaFP2; antifungal protein; AFP2; ss.

Synthetic.

Dahlia merckii.

Unidentified.

Key Location/Qualifiers  
3.437  
/\*tag= a  
/product= "fusion protein of DmAMP1 and RsaFP2"

WO200011175-A1.

02-MAR-2000.

17-AUG-1999; 99WO-GB002716.

18-AUG-1998; 98GB-00018001.

04-DEC-1998; 98GB-00026753.

(ZENNE ) ZENNECA LTD.

Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;

WPI; 2000-246564/21.

P-PSDB; AAY84062.

Improving expression of polypeptides in plants involves coexpression of  
two or more proteins in plants within a single transcription unit.

XX Disclosure; Fig 24; 151pp; English.

XX The present sequence encodes a protein of the invention, comprising the

XX mature proteins of the plant defensins, the Dahlia antimicrobial protein

CC (AMP) 1 and the antifungal protein 2 (AFP2), linked by a linker

CC propeptide of the invention. The specification describes methods for

CC improving expression levels of one or more proteins in a transgenic

CC plant. The method comprises inserting a DNA sequence having a promoter

CC region operably linked to two or more protein encoding regions separated

CC by a DNA sequence coding for a linker propeptide and a terminator region.

CC The method is used to produce proteins in plants. The linker propeptide

CC comprising a cleavage site, whereby the expressed polypeptide is post-

CC translationally processed into the component protein molecules. The

CC propeptide sequence is rich in amino acids A, V, S and T and contains

CC dipeptidic sequences consisting of either two acidic, two basic or one

CC acidic and one basic residue as a cleavable linker sequence  
XX

SO Sequence 446 BP; 111 A; 102 C; 123 G; 110 T; 0 U; 0 Other;

Query Match 38.6%; Score 172.2; DB 3; Length 446;

Best Local Similarity 93.3%; Pred. No. 2.7e-37;  
Matches 180; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

155 AGATATGCGATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214

65 AGATATGCGATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 124

215 CTGTGGCAATACCGGACATTTGTGACCAACCAATGTAATCATGGAGGGTCCGCTCACGG 274

125 CTGTGGCAATACCGGACATTTGTGACCAACCAATGTAATCATGGAGGGTCCGCTCACGG 184

275 AGCGTGTATGTCGCTGTAACCGGAAACACATGTTTCTGTTACTTCAATTGTAATAAAGC 334

185 AGCGTGTATGTCGCTGTAACCGGAAACACATGTTTCTGTTACTTCAATTGTAACGCGC 244

335 CGAAAGCTGCTCAAGACAACTTAAG---CCGACCACTGCTCAAGACAACTTA 347

245 CGACGAGTGGCT 257

Db

RESULT 13

ID AA299334 standard; DNA; 1093 BP.

AA299334;

03-JUL-2000 (first entry)

DNA encoding a fusion protein of DmAMP1, RsaFP2, HsaFP1 and AceAMP1.

Antimicrobial protein; AMP1; transgenic plant; linker propeptide;  
KW protein expression; plant defensin; RsaFP2; antifungal protein; AFP2; ss.

Synthetic.

Dahlia merckii.

Unidentified.

Key Location/Qualifiers  
3.1085  
/\*tag= a  
/product= "fusion protein of plant defensins"

WO200011175-A1.

02-MAR-2000.

17-AUG-1999; 99WO-GB002716.

18-AUG-1998; 98GB-00018001.

04-DEC-1998; 98GB-00026753.

(ZENNE ) ZENNECA LTD.



```

XX PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
XX WPI: 2000-246564/21.
XX P-PSDB: AAY64057.
XX DR
XX PT Improving expression of polyproteins in plants involves coexpression of
XX two or more proteins in plants within a single transcription unit.
XX PS Disclosure; Fig 29; 151pp; English.
XX CC The present sequence encodes a protein of the invention, comprising the
XX mature proteins of the plant defensins, the Dahlia antimicrobial protein
XX (AMP) 1, antifungal protein 2 (RAFP2), HsAFP1, and AceAMP1, linked by
XX linker propeptides of the invention. The specification describes methods
XX for improving expression levels of one or more proteins in a transgenic
XX plant. The method comprises inserting a DNA sequence having a promoter
XX region operably linked to two or more protein encoding regions separated
XX by a DNA sequence coding for a linker propeptide and a terminator region.
XX The method is used to produce proteins in plants. The linker propeptide
XX comprising a cleavage site, whereby the expressed polypeptide is post-
XX translationally processed into the component protein molecules. The
XX propeptide sequence is rich in amino acids A, V, S and T and contains
XX dipeptidic sequences consisting of either two acidic, two basic or one
XX acidic and one basic residue as a cleavable linker sequence
XX
SQ Sequence 1093 BP; 278 A; 271 C; 287 G; 257 T; 0 U; 0 Other;
Query Match 38.1%; Score 170; DB 3; Length 1093;
Best Local Similarity 84.3%; Pred. No. 1.5e-36;
Matches 204; Conservative 0; Mismatches 35; Indels 3; Gaps 1;
QY 155 AGATATGCAATCCGTTAGTGAAGAACTATGCGAAGAACTGCAAGCATGTCGGGAAA 214
DB 65 AGATATGCAATCCGTTAGTGAAGAACTATGCGAAGAACTGCAAGCATGTCGGGAAA 124
QY 215 CTGTGGCAATACGGGACATTGTGCAACCAATGTAATCATAGGAGGTGCGCCCATGG 274
DB 125 CTGTGGCAACACGGGACATTGTGCAACCAATGTAATCATAGGAGGTGCGCCCATGG 184
QY 275 AGCGTGTCATGTGGTGAACGGGAAACACATGTGTTCTGTTACTTCAATTGTAAAAAGC 334
DB 185 AGCGTGTCATGTGGTGAACGGGAAACACATGTGTTCTGTTACTTCAATTGTAAAAAGC 244
QY 335 CGAAGAACTGCTCAAGACAACTTAAG---CCGAAACAATCGCTCAAGACAACTTAA 391
DB 245 TGAGGAAGCTGCTGCTGCTATTCTGAAGCTTGTGAAGAACTTCTCAAGAAAGCTCC 304
QY 392 TG 393
DB 305 TG 306

RESULT 14
AA299324
ID AA299324 standard; DNA; 522 BP.
XX AA299324;
XX
XX 03-JUL-2000 (first entry)
XX
XX DNA encoding a fusion protein of DmAMP1 and RAFP2.
XX
XX Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
XX protein expression; plant defensin; RAFP2; antifungal protein; AFP2; BS.
XX
XX Synthetic.
XX OS Dahlia merckii.
XX OS Unidentified.
XX
XX Key Location/Qualifiers
XX misc_feature 160..309
XX /tag= a

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```

FT FT /note= "encodes DmAMP1"
FT FT misc_feature 358..510
FT FT /tag= b
FT FT /note= "encodes RAFP2"
XX
XX W0200011175-A1.
XX
XX 02-MAR-2000.
XX
XX 17-AUG-1999; 99WC-GB002716.
XX
XX 18-AUG-1998; 98GB-00018001.
XX
XX 04-DEC-1998; 98GB-00026753.
XX
XX (ZENEC) ZENEC LTD.
XX
XX PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
XX WPI: 2000-246564/21.
XX P-PSDB: AAY64057.
XX
XX DR Improving expression of polyproteins in plants involves coexpression of
XX two or more proteins in plants within a single transcription unit.
XX
XX PS Example 2; Fig 8; 151pp; English.
XX
XX CC The present sequence encodes a protein of the invention, comprising the
XX mature proteins of the plant defensins, the Dahlia antimicrobial protein
XX (AMP) 1 and the antifungal protein 2 (RAFP2), linked by a linker
XX propeptide of the invention. The specification describes methods for
XX improving expression levels of one or more proteins in a transgenic
XX plant. The method comprises inserting a DNA sequence having a promoter
XX region operably linked to two or more protein encoding regions separated
XX by a DNA sequence coding for a linker propeptide and a terminator region.
XX The method is used to produce proteins in plants. The linker propeptide
XX comprising a cleavage site, whereby the expressed polypeptide is post-
XX translationally processed into the component protein molecules. The
XX propeptide sequence is rich in amino acids A, V, S and T and contains
XX dipeptidic sequences consisting of either two acidic, two basic or one
XX acidic and one basic residue as a cleavable linker sequence
XX
SQ Sequence 522 BP; 147 A; 119 C; 127 G; 129 T; 0 U; 0 Other;
Query Match 37.9%; Score 169.2; DB 3; Length 522;
Best Local Similarity 95.6%; Pred. No. 1.9e-36;
Matches 174; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 155 AGATATGCAATCCGTTAGTGAAGAACTATGCGAAGAACTGCAAGCATGTCGGGAAA 214
DB 138 AGATATGCAATCCGTTAGTGAAGAACTATGCGAAGAACTGCAAGCATGTCGGGAAA 197
QY 215 CTGTGGCAATACGGGACATTGTGCAACCAATGTAATCATAGGAGGTGCGCCCATGG 274
DB 198 CTGTGGCAACACGGGACATTGTGCAACCAATGTAATCATAGGAGGTGCGCCCATGG 257
QY 275 AGCGTGTCATGTGGTGAACGGGAAACACATGTGTTCTGTTACTTCAATTGTAAAAAGC 334
DB 258 AGCGTGTCATGTGGTGAACGGGAAACACATGTGTTCTGTTACTTCAATTGTAAAAAGC 317
QY 335 CG 336
DB 318 TG 319

RESULT 15
AA54387
ID AA54387 standard; DNA; 460 BP.
XX AA54387;
XX
XX 11-APR-2001 (first entry)
XX
XX Plant defensin coding sequence.

```

```
XX      Defensin; disease; fungus; resistance; transgenic plant; vaccine;
KW      Immunisation; antibody; crop protection; db.
OS      Dimorphotheca sinuata.
XX      Key      Location/Qualifiers
FT      CDS      25..351
FT      /tag= a
FT      /product= "Plant defensin"
XX      MO200068405-A2.
XX      16-NOV-2000.
XX      PD
XX      PF      03-MAY-2000; 2000MO-US011952.
XX      PR      07-MAY-1999; 99US-0133039P.
XX      PA      (DUPO ) DU PONT DE NEMOURS & CO E I.
XX      PI      Miao G, Wang Z, Famodu OO;
XX      DR      WPI; 2001-024871/03.
XX      DR      P-PSDB; AAB04046.
XX      PT      Isolated polynucleotides encoding plant defensins, useful for creating
XX      PT      transgenic plants with higher or lower levels of defensin polypeptides,
XX      PT      especially for increasing disease (e.g. fungal) resistance and stress
XX      PT      tolerance.
XX      PS      Claim 2; Page 37; 50pp; English.
XX      CC      Nucleotides encoding plant defensins can be used to create transgenic
XX      CC      plants in which plant defensin polypeptides are present at higher or
XX      CC      lower levels than normal, or in cell types or developmental stages in
XX      CC      which they are not normally found. This has the effect of altering the
XX      CC      level of disease (e.g. fungal) resistance and stress tolerance in those
XX      CC      cells. The defensin polypeptides are useful for immunising animals to
XX      CC      produce polyclonal or monoclonal antibodies. These antibodies are useful
XX      CC      for screening cDNA expression libraries to isolate full-length plant
XX      CC      defensin cDNA clones
XX      SQ      Sequence 460 BP; 160 A; 83 C; 102 G; 115 T; 0 U; 0 Other;
XX
Query Match      37.8%; Score 168.6; DB 5; Length 460;
Best Local Similarity 81.6%; Pred. No. 2.6e-36;
Matches 195; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
QY      155 AGATATGGCATCCGTTAGTGGAGAACTATGCGAAGCTAGCAAGCATGTCGGGAA 214
DB      87 AGAAATCGCACTGTGAGAGTGCACATATGTGAGAAAGCTAGCAAGCATGTCAGGCAA 146
QY      215 CTGTGGCAATACGGGACATTGTGCAACCAATGTAATCATGGAGGGTCCGCCCATGG 274
DB      147 CTGTGGCAACACGGGACACTGTGACGACAGCTGTAAGTCTGTGGAGACTCAAGCCCATGG 206
QY      275 AGCGTGTCTATGTGGTGAACGGGAAACACATGTGTTCTGTTACTTCAATTGTAAGG 334
DB      207 TCGGTGTCTATGTGGTGAACGGGAAACACATGTGTTCTGTTACTTCAATTGTAAGG 266
QY      335 CGAAAGCTTGTCAAGACAACTTAAGCCGAACAACTGGCTCAAGACAACTTAATG 393
DB      267 CGAAAGCTTGTCAAGACAACTTAAGCCGAACAACTGGCTCAAGACAACTTAATG 325
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Search completed: March 18, 2005, 13:52:15  
Job time : 388 secs

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OM nucleic - nucleic search, using bw model

Run on: March 18, 2005, 06:59:55 ; Search time 2319 Seconds  
(without alignments)  
9319.114 Million cell updates/sec

Title: US-09-763-019-5

Perfect score: 446

Sequence: 1 atggcgaacgcgtcgtcgtc.....ctccaacgtcgaacatccg 446

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_hcg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pac: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_scs: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_y1: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	446	100.0	446	6	BD223232 Method of
2	446	100.0	446	6	BD240919 Polynucle
3	287.2	64.4	606	6	BD223236 Method of
4	284	63.7	557	6	BD223246 Method of
5	215.2	48.3	534	6	BD223234 Method of
6	215.2	48.3	534	6	BD240936 Polynucle
7	212	47.5	485	6	BD223245 Method of
8	177.2	39.7	577	6	BD240918 Polynucle
9	173.2	38.8	485	6	BD223243 Method of
10	173.2	38.6	446	6	BD223239 Method of
11	170	38.1	1093	6	BD223244 Method of
12	169.2	37.9	522	6	BD223233 Method of
13	168.6	37.8	460	6	AX046745 Sequence
14	167.2	37.5	534	6	AX046743 Sequence
15	167.2	37.5	534	6	BD223237 Method of
16	166	37.2	437	6	BD223242 Method of
17	166	37.2	437	6	BD223241 Method of
18	166	37.2	443	6	BD223240 Method of
19	166	37.2	488	6	BD223248 Method of

20	166	37.2	575	6	BD223249 Method of
21	165.6	37.1	316	6	BD223238 Method of
22	165.6	37.1	316	6	BD240937 Polynucle
23	164	36.8	485	6	BD223247 Method of
24	157.8	35.4	523	6	BD240916 Polynucle
25	156.4	35.1	457	6	AX046755 Sequence
26	156.4	35.1	463	6	AX046751 Sequence
27	156.4	35.1	603	6	AX046753 Sequence
28	154.8	34.7	458	6	AX046763 Sequence
29	154.8	34.7	460	6	AX046759 Sequence
30	154.2	34.6	558	8	AF346865 Helianthu
31	154.2	34.6	565	6	AR452919 Sequence
32	154.2	34.6	565	6	AX060648 Sequence
33	153.2	34.3	464	6	AX046761 Sequence
34	153.2	34.3	472	6	AX046765 Sequence
35	146.8	32.9	399	6	BD240915 Polynucle
36	138.4	31.0	439	6	AX046757 Sequence
37	138.4	30.1	385	6	BD240917 Polynucle
38	120.2	27.0	126	6	BD240922 Polynucle
39	99.4	22.3	150	6	A26963 D.merkli AM
40	99.4	22.3	150	6	A39543 Sequence 31
41	99.4	22.3	150	6	AR050143 Sequence
42	98.4	22.3	150	6	AR130262 Sequence
43	99.4	22.3	150	6	BD240920 Polynucle
44	99.4	22.3	150	6	I23718 Sequence 31
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## ALIGNMENTS

RESULT 1  
BD223232 446 bp DNA linear PAT 17-JUL-2003  
LOCUS Method of genetic expression of polypeptide in plant.

DEFINITION BD223232  
ACCESSION BD223232.1 GI:33033002  
VERSION JP 2002523047-A/1.  
KEYWORDS Dahlia merckii (bedding dahlia)  
SOURCE Dahlia merckii  
ORGANISM Dahlia merckii

REFERENCE  
1 (bases 1 to 446)  
Broekert, W.F., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and Ray, J.A.  
Method of genetic expression of polypeptide in plant  
Patent: JP 2002523047-A 1 30-JUL-2002;  
JOURNAL SYNGENTA LTD

AUTHORS  
Ray, J.A.  
TITLE  
Method of genetic expression of polypeptide in plant  
COMMENT  
OS Dahlia merckii  
PN JP 2002523047-A/1  
PD 30-JUL-2002 JP 2000566429  
PF 17-AUG-1999 JP 2000566429  
PR 18-AUG-1998 GB 9818001.1 04-DEC-1998 GB 9826753.7 PI  
WILHELM FRANS BROEKERT, ISABELLE ELISA JEANNE  
AUGUSTINE FRANCOIS,  
PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI

PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P1/02//C12N5/10, PC  
C12R1.91,  
PC C12N15/00, C12N5/00, (C12N5/00, C12R1.91)  
CC Method of genetic expression of polypeptide in plant FH Key  
FT CDS  
CDS Location/Qualifiers  
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(157)..(446).

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source location/Qualifiers  
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ORIGIN

Query Match 100.0%; Score 446; DB 6; Length 446;  
Best Local Similarity 100.0%; Pred. No. 7.4e-105;  
Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGGGATCGGTCGGTTCGGGCTTCGTTGATCCCTTTCGTCGCCATC 60  
DB 1 ATGGGATCGGTCGGTTCGGGCTTCGTTGATCCCTTTCGTCGCCATC 60  
OY 61 TCAGGTATCAAACTTTAGTTCAATTTATGAAATGATATTATTTATATG 120  
DB 61 TCAGGTATCAAACTTTAGTTCAATTTATGAAATGATATTATTTATATG 120  
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DB 121 TTTTATGTTCTGCAAGTTGCCAAATTTAGTATGATATGCAATCCGTAGTGAAGAC 180  
OY 181 TATCGGAGAAAGCTAGCAAGACATGTCGGGAAACTGTGGCAATACGGGACATTGTGACA 240  
DB 181 TATCGGAGAAAGCTAGCAAGACATGTCGGGAAACTGTGGCAATACGGGACATTGTGACA 240  
OY 241 ACCAATGTAATCATGGAGGGTGGGCGCATGAGCGTGCATGTGCTAAACGGGAAAC 300  
DB 241 ACCAATGTAATCATGGAGGGTGGGCGCATGAGCGTGCATGTGCTAAACGGGAAAC 300  
OY 301 ACATGTGTTCTGTTACTTCAATTTGTAAAAAGCCGAAAGCTTGTCAAGACAACTTA 360  
DB 301 ACATGTGTTCTGTTACTTCAATTTGTAAAAAGCCGAAAGCTTGTCAAGACAACTTA 360  
OY 361 AAGCCGAACAACCTGCTCAAGACAACTTAATGCCCAAGCTTGACCGTGACCAAGA 420  
DB 361 AAGCCGAACAACCTGCTCAAGACAACTTAATGCCCAAGCTTGACCGTGACCAAGA 420  
OY 421 AAGTGTTCCAAACGTTGAACATCCG 446  
DB 421 AAGTGTTCCAAACGTTGAACATCCG 446

RESULT 2  
BD240919 446 bp DNA linear PAT 17-JUL-2003  
LOCUS Polynucleotide sequences.  
DEFINITION BD240919.1 GI:33050689  
ACCESSION BD240919.1 GI:33050689  
VERSION JP 2002523052-A/5.  
KEYWORDS Dahlia merckii (bedding dahlia)  
SOURCE Dahlia merckii  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Coreoideae; Dahlia.  
REFERENCE 1 (bases 1 to 446)  
AUTHORS Evans,I.J. and Ray,J.A.  
TITLE Polynucleotide sequences  
JOURNAL Patent: JP 2002523052-A 5 30-JUL-2002;  
SYNGENTA LTD  
COMMENT OS Dahlia merckii (dahlia)  
PN JP 2002523052-A/5  
PD 30-JUL-2002  
PF 17-AUG-1999 JP 2000566448  
PR 18-AUG-1998 GB 9818003.7  
PI IAN JEFFREY EVANS,JOHN ANTHONY RAY  
PC C12N15/09,A01H5/00,C07K14/415,C12N5/10//C12N5/10,C12R1:91),  
PC C12N15/00,  
CC C12N5/00,(C12N5/00,C12R1:91)  
CDS Polynucleotide sequences  
FH Key Location/Qualifiers  
FT CDS (1)..(64).  
Location/Qualifiers  
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ORIGIN  
Query Match 100.0%; Score 446; DB 6; Length 446;  
Best Local Similarity 100.0%; Pred. No. 7.4e-105;  
Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGGGATCGGTCGGTTCGGGCTTCGTTGATCCCTTTCGTCGCCATC 60  
DB 1 ATGGGATCGGTCGGTTCGGGCTTCGTTGATCCCTTTCGTCGCCATC 60  
OY 61 TCAGGTATCAAACTTTAGTTCAATTTATGAAATGATATTATTTATATG 120  
DB 61 TCAGGTATCAAACTTTAGTTCAATTTATGAAATGATATTATTTATATG 120  
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DB 121 TTTTATGTTCTGCAAGTTGCCAAATTTAGTATGATATGCAATCCGTAGTGAAGAC 180  
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OY 241 ACCAATGTAATCATGGAGGGTGGGCGCATGAGCGTGCATGTGCTAAACGGGAAAC 300  
DB 241 ACCAATGTAATCATGGAGGGTGGGCGCATGAGCGTGCATGTGCTAAACGGGAAAC 300  
OY 301 ACATGTGTTCTGTTACTTCAATTTGTAAAAAGCCGAAAGCTTGTCAAGACAACTTA 360  
DB 301 ACATGTGTTCTGTTACTTCAATTTGTAAAAAGCCGAAAGCTTGTCAAGACAACTTA 360  
OY 361 AAGCCGAACAACCTGCTCAAGACAACTTAATGCCCAAGCTTGACCGTGACCAAGA 420  
DB 361 AAGCCGAACAACCTGCTCAAGACAACTTAATGCCCAAGCTTGACCGTGACCAAGA 420  
OY 421 AAGTGTTCCAAACGTTGAACATCCG 446  
DB 421 AAGTGTTCCAAACGTTGAACATCCG 446

RESULT 3  
BD223236 606 bp DNA linear PAT 17-JUL-2003  
LOCUS Method of genetic expression of polypeptide in plant.  
DEFINITION BD223236  
ACCESSION BD223236.1 GI:33033006  
VERSION JP 2002523047-A/5.  
KEYWORDS synthetic construct  
SOURCE other sequences; artificial sequences.  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 606)  
AUTHORS Broekert,W.F., Francois,I.E.J.A., Bolle,M.F.C.D., Evans,I.J. and Ray,J.A.  
TITLE Method of genetic expression of polypeptide in plant  
JOURNAL Patent: JP 2002523047-A 5 30-JUL-2002;  
SYNGENTA LTD  
COMMENT OS Artificial Sequence  
PN JP 2002523047-A/5  
PD 30-JUL-2002  
PF 17-AUG-1999 JP 2000566429  
PR 18-AUG-1998 GB 9818001.1,04-DEC-1998 GB 9826753.7 PI  
PI WILLEM FRANS BROEKERT,ISABELLE ELSA JEANNE  
PI AUGUSTINE FRANCOIS,  
PI MIGUEL FRANCESCO COLETA DE BOLLE,IAN JEFFREY EVANS,JOHN PI  
ANTHONY RAY  
PC C12N15/09,A01H1/00,C07K12,C12N5/10,C12P21/02//C12N5/10,PC  
PC C12N15/00,C12N5/00,(C12N5/00,C12R1:91)  
CC Description of Artificial Sequence: Synthetic sequence FH  
FH Key Location/Qualifiers  
FT CDS (76)..(597).  
Location/Qualifiers  
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ORIGIN

Query Match 64.4%; Score 287.2; DB 6; Length 606;  
Best Local Similarity 99.0%; Pred. No. 1.1e-63;  
Matches 289; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214  
DB 138 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 197  
QY 215 CTGTGGCAATACGGGACATTTGTGACAACTGTAATCATGGAGGGTGGCCCATGG 274  
DB 198 CTGTGGCAACACGGGACATTTGTGACAACTGTAATCATGGAGGGTGGCCCATGG 257  
QY 275 AGCGTGCATGTGGGTAAACGGGAAACACATGTGTTCTGTTACTTCAATTGTAAAGAAC 334  
DB 258 AGCGTGCATGTGGGTAAACGGGAAACACATGTGTTCTGTTACTTCAATTGTAAAGAAC 317

QY 335 CGAAAAGCTTGCTCAAGCAAACTTAAAGCCGAAACATCGCTCAAGCAAACTTAATGC 394  
DB 318 CGAAAAGCTTGCTCAAGCAAACTTAAAGCCGAAACATCGCTCAAGCAAACTTAATGC 377

QY 395 CGAAAAGCTTGACCGGTGATGCGCAAGAAAGTGTTCCAAACGTTGAACATCCG 446  
DB 378 CGAAAAGCTTGACCGGTGATGCGCAAGAAAGTGTTCCAAACGTTGAACATCCG 429

RESULT 4  
BD223246 557 bp DNA linear PAT 17-JUL-2003  
LOCUS Method of genetic expression of polyprotein in plant.  
DEFINITION BD223246  
ACCESSION BD223246  
VERSION BD223246.1 GI:33033016  
KEYWORDS JP 2002523047-A/15.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 557)  
AUTHORS Broekaert, W.F., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and Ray, J.A.  
TITLE Method of genetic expression of polyprotein in plant  
JOURNAL Patent: JP 2002523047-A 15 30-JUL-2002;  
COMMENT OS Artificial Sequence  
PN JP 2002523047-A/15  
PD 30-JUL-2002  
PF 17-AUG-1999 JP 2000566429  
PR 18-AUG-1998 GB 9818001.1 04-DEC-1998 GB 9826753.7 PI  
WILLEM FRANS BROEKAERT, ISABELLE ELSA JEANNE  
AUGUSTINE FRANCOIS,  
PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI  
ANTHONY RAY  
PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P21/02//C12N5/10, PC  
C12R1:91,  
CC C12N15/00, C12N5/00, (C12N5/00, C12R1:91)  
CDS Description of Artificial Sequence: Synthetic sequence FH  
Key Location/Qualifiers  
FT CDS Location/Qualifiers (3)..(548).

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ORIGIN

Query Match 63.7%; Score 284; DB 6; Length 557;  
Best Local Similarity 98.3%; Pred. No. 7.6e-63;  
Matches 287; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214  
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QY 215 CTGTGGCAATACGGGACATTTGTGACAACTGTAATCATGGAGGGTGGCCCATGG 274  
DB 198 CTGTGGCAACACGGGACATTTGTGACAACTGTAATCATGGAGGGTGGCCCATGG 257  
QY 275 AGCGTGCATGTGGGTAAACGGGAAACACATGTGTTCTGTTACTTCAATTGTAAAGAAC 334  
DB 258 AGCGTGCATGTGGGTAAACGGGAAACACATGTGTTCTGTTACTTCAATTGTAAAGAAC 317

DB 65 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGCAA 124  
QY 215 CTGTGGCAATACGGGACATTTGTGACAACTGTAATCATGGAGGGTGGCCCATGG 274  
DB 125 CTGTGGCAACGGGACATTTGTGACAACTGTAATCATGGAGGGTGGCCCATGG 184  
QY 275 AGCGTGCATGTGGGTAAACGGGAAACACATGTGTTCTGTTACTTCAATTGTAAAGAAC 334  
DB 185 AGCGTGCATGTGGGTAAACGGGAAACACATGTGTTCTGTTACTTCAATTGTAAAGAAC 244

QY 335 CGAAAAGCTTGCTCAAGCAAACTTAAAGCCGAAACATCGCTCAAGCAAACTTAATGC 394  
DB 245 CGAAAAGCTTGCTCAAGCAAACTTAAAGCCGAAACATCGCTCAAGCAAACTTAATGC 304

QY 395 CGAAAAGCTTGACCGGTGATGCGCAAGAAAGTGTTCCAAACGTTGAACATCCG 446  
DB 305 CGAAAAGCTTGACCGGTGATGCGCAAGAAAGTGTTCCAAACGTTGAACATCCG 356

RESULT 5  
BD223234 534 bp DNA linear PAT 17-JUL-2003  
LOCUS Method of genetic expression of polyprotein in plant.  
DEFINITION BD223234  
ACCESSION BD223234  
VERSION BD223234.1 GI:33033004  
KEYWORDS JP 2002523047-A/3.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 534)  
AUTHORS Broekaert, W.F., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and Ray, J.A.  
TITLE Method of genetic expression of polyprotein in plant  
JOURNAL Patent: JP 2002523047-A 3 30-JUL-2002;  
COMMENT OS Artificial Sequence  
PN JP 2002523047-A/3  
PD 30-JUL-2002  
PF 17-AUG-1999 JP 2000566429  
PR 18-AUG-1998 GB 9818001.1 04-DEC-1998 GB 9826753.7 PI  
WILLEM FRANS BROEKAERT, ISABELLE ELSA JEANNE  
AUGUSTINE FRANCOIS,  
PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI  
ANTHONY RAY  
PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P21/02//C12N5/10, PC  
C12R1:91,  
CC C12N15/00, C12N5/00, (C12N5/00, C12R1:91)  
CDS Description of Artificial Sequence: Synthetic sequence FH  
Key Location/Qualifiers  
FT CDS Location/Qualifiers (76)..(525).

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/db\_xref="taxon:32630"

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Query Match 48.3%; Score 215.2; DB 6; Length 534;  
Best Local Similarity 98.6%; Pred. No. 5.2e-45;  
Matches 217; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 155 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 214  
DB 138 AGATATCGCATCCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAAA 197  
QY 215 CTGTGGCAATACGGGACATTTGTGACAACTGTAATCATGGAGGGTGGCCCATGG 274  
DB 198 CTGTGGCAACACGGGACATTTGTGACAACTGTAATCATGGAGGGTGGCCCATGG 257  
QY 275 AGCGTGCATGTGGGTAAACGGGAAACACATGTGTTCTGTTACTTCAATTGTAAAGAAC 334  
DB 258 AGCGTGCATGTGGGTAAACGGGAAACACATGTGTTCTGTTACTTCAATTGTAAAGAAC 317

QY 335 CGAAAGCTTGCTCAAGCAAACTTAAGCCGAACAATC 374  
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 DB 318 CGAAAGCTTGCTCAAGCAAACTTAAGCCGAACAATC 357

RESULT 6  
 BD240936 534 bp DNA linear PAT 17-JUL-2003

LOCUS BD240936  
 DEFINITION Polynucleotide sequences.  
 ACCESSION BD240936  
 VERSION BD240936.1 GI:33050706  
 KEYWORDS JP 2002523052-A/22.  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.  
 1 (bases 1 to 534)  
 AUTHORS Evans, I.J. and Ray, J.A.  
 TITLE Polynucleotide sequences  
 JOURNAL Patent: JP 2002523052-A 22 30-JUL-2002;  
 SYNGENTA LTD  
 COMMENT OS Artificial Sequence  
 PN JP 2002523052-A/22  
 PD 30-JUL-2002  
 PF 17-AUG-1999 JP 2000566448  
 PR 18-AUG-1998 GB 9818003.7  
 PI IAN JEFFREY EVANS, JOHN ANTHONY RAY  
 PC C12N15/09,A01H5/00,C07K14/415,C12N5/10//C12N5/10,C12R1:91,  
 PC C12N5/00,C12N5/00,C12R1:91  
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 Best Local Similarity 98.6%; Pred. No. 5.2e-45;  
 Matches 217; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 155 AGATATGCAATCCGTTAGTGAAGAACTATGCGAAGAACTGCAAGACATGTCGGGAAA 214  
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 DB 138 AGATATGCAATCCGTTAGTGAAGAACTATGCGAAGAACTGCAAGACATGTCGGGCAA 197

QY 215 CTGTGGCAATACGGGACATTTGACCAACCAATGTAATCATGGAGGGTGGGCCATGG 274  
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 DB 198 CTGTGGCAACCGGACATTTGACCAACCAATGTAATCATGGAGGGTGGGCCATGG 257

QY 275 AGCGTGTATGTGCGTAAACGGGAAACACATGTGTTCTGTTACTTCAATTGTAAAAAGC 334  
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 DB 258 AGCGTGTATGTGCGTAAACGGGAAACACATGTGTTCTGTTACTTCAATTGTAAAAAGC 317

QY 335 CGAAAGCTTGCTCAAGCAAACTTAAGCCGAACAATC 374  
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 DB 318 CGAAAGCTTGCTCAAGCAAACTTAAGCCGAACAATC 357

RESULT 7  
 BD223245 485 bp DNA linear PAT 17-JUL-2003

LOCUS BD223245  
 DEFINITION Method of genetic expression of polypeptide in plant.  
 ACCESSION BD223245  
 VERSION BD223245.1 GI:33033015  
 KEYWORDS JP 2002523047-A/14.  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.  
 1 (bases 1 to 485)  
 AUTHORS Broekert, W.F., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and Ray, J.A.

TITLE Method of genetic expression of polypeptide in plant  
 JOURNAL Patent: JP 2002523047-A 14 30-JUL-2002;  
 SYNGENTA LTD  
 COMMENT OS Artificial Sequence  
 PN JP 2002523047-A/14  
 PD 30-JUL-2002  
 PF 17-AUG-1999 JP 2000566429  
 PR 18-AUG-1998 GB 9818001.1, 04-DEC-1998 GB 9826753.7 PI  
 WILLEM FRANS BROEKERT, ISABELLE ELISA JEANNE  
 AUGUSTINE FRANCOIS,  
 PI MIGUEL FRANCISCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI  
 ANTHONY RAY  
 PC C12N15/09,A01H1/00,C07K12/12,C12N5/10,C12P21/02//C12N5/10, PC  
 C12R1:91,  
 PC C12N15/00,C12N5/00,C12N5/00,C12R1:91  
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 Best Local Similarity 97.7%; Pred. No. 3.5e-44;  
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 DB 65 AGATATGCAATCCGTTAGTGAAGAACTATGCGAAGAACTGCAAGACATGTCGGGCAA 124

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 DB 125 CTGTGGCAACCGGACATTTGACCAACCAATGTAATCATGGAGGGTGGGCCATCGG 184

QY 275 AGCGTGTATGTGCGTAAACGGGAAACACATGTGTTCTGTTACTTCAATTGTAAAAAGC 334  
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 DB 185 AGCGTGTATGTGCGTAAACGGGAAACACATGTGTTCTGTTACTTCAATTGTAAAAAGC 244

QY 335 CGAAAGCTTGCTCAAGCAAACTTAAGCCGAACAATC 374  
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 DB 245 CGAAAGCTTGCTCAAGCAAACTTAAGCCGAACAATC 284

RESULT 8  
 BD240918 577 bp DNA linear PAT 17-JUL-2003

LOCUS BD240918  
 DEFINITION Polynucleotide sequences.  
 ACCESSION BD240918  
 VERSION BD240918.1 GI:33050688  
 KEYWORDS JP 2002523052-A/4.  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.  
 1 (bases 1 to 577)  
 AUTHORS Evans, I.J. and Ray, J.A.  
 TITLE Polynucleotide sequences  
 JOURNAL Patent: JP 2002523052-A 4 30-JUL-2002;  
 SYNGENTA LTD  
 COMMENT OS Artificial Sequence  
 PN JP 2002523052-A/4  
 PD 30-JUL-2002  
 PF 17-AUG-1999 JP 2000566448  
 PR 18-AUG-1998 GB 9818003.7  
 PI IAN JEFFREY EVANS, JOHN ANTHONY RAY  
 PC C12N15/09,A01H5/00,C07K14/415,C12N5/10//C12N5/10,C12R1:91,  
 PC C12N5/00,C12N5/00,C12R1:91

CC Polynucleotide sequences  
 FH Key Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:43367"

## ORIGIN

Query Match 39.7%; Score 177.2; DB 6; Length 577;  
 Best Local Similarity 80.1%; Pred. No. 3.7e-35;  
 Matches 234; Conservative 0; Mismatches 28; Indels 30; Gaps 1;

OY 155 AGATATGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAA 214  
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 DB 82 AGATATCCAAAGTGTGAGAGAGAGATGCGAGAAAGCTAGCAAGACATGTCGGGAA 141  
 OY 215 CTGTGGCAATACGGGACATTTGTGACCAACCAATGTAATCATGGAGGGTGGCCCATGG 274  
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 DB 142 CTGTGGCAATACGGGACATTTGTGACCAACCAATGTAATCATGGAGGGTGGCCCATGG 201  
 OY 275 AGCGTGTATGTGCGTAAACGGGAAACACATGTTCTTCTTACTTCAATTGTAATAAAC 334  
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 DB 202 GCGGTGCCACGTCGTGGAGGAAACACATGTTCTTCTTACTTCAATTGTTCCCAAGC 261  
 OY 335 CGAAAGCTTGCTCAAGCAAACTTAAGCCGAAACAATCGCTCAAGCAAACTTAATGC 394  
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 DB 262 CGAAAGCTT-----GCTCAAGCAAAAGTTAATGC 291  
 OY 395 CGAAAGCTTGACCGTGTATGCGCAAGAAAGTGTTCAAACGTTGAACATCCG 446  
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 DB 292 CCAAGAGCTTGACCGTGTATGCGCAAGAAAGTGTTCGAAACGTTGAACATCCG 343

RESULT 9  
 BD223243 485 bp DNA linear PAT 17-JUL-2003  
 LOCUS Method of genetic expression of polypeptide in plant.  
 DEFINITION BD223243  
 ACCESSION BD223243.1 GI:33033013  
 VERSION JP 2002523047-A/12.  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 other sequences; artificial sequences.  
 1 (bases 1 to 485)  
 Broekaert, W.F., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and Ray, J.A.  
 Ray, J.A.  
 Method of genetic expression of polypeptide in plant  
 Patent: JP 2002523047-A 12 30-JUL-2002;  
 SYNGENTA LTD  
 COMMENT  
 OS Artificial Sequence  
 PN JP 2002523047-A/12  
 PD 30-JUL-2002  
 PF 17-AUG-1999 JP 2000566429  
 PR 18-AUG-1998 GB 9818001.1 04-DEC-1998 GB 9826753.7 PI  
 WILLEM FRANS BROEKAERT, ISABELLE ELISA JEANNE  
 AUGUSTINE FRANCOIS,  
 PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI  
 ANTHONY RAY  
 PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P21/02//C12N5/10, PC  
 C12R1:91),  
 CC Description of Artificial Sequence: Synthetic sequence FH  
 Key Location/Qualifiers  
 FT CDS (3) .. (476).

## FEATURES

## source

1..485  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"

## ORIGIN

Query Match 38.8%; Score 173.2; DB 6; Length 485;  
 Best Local Similarity 85.1%; Pred. No. 4e-34;  
 Matches 206; Conservative 0; Mismatches 33; Indels 3; Gaps 1;

OY 155 AGATATGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAA 214  
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 DB 65 AGATATGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAA 124  
 OY 215 CTGTGGCAATACGGGACATTTGTGACCAACCAATGTAATCATGGAGGGTGGCCCATGG 274  
 |||||  
 DB 125 CTGTGGCAATACGGGACATTTGTGACCAACCAATGTAATCATGGAGGGTGGCCCATGG 184  
 OY 275 AGCGTGTATGTGCGTAAACGGGAAACACATGTTCTTCTTACTTCAATTGTAATAAAC 334  
 |||||  
 DB 185 AGCGTGTATGTGCGTAAACGGGAAACACATGTTCTTCTTACTTCAATTGTTGCTAAC 244  
 OY 335 CGAAAGCTTGCTCAAGCAAACTTAAG---CGAACAATCGCTCAAGCAAACTTA 391  
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 DB 245 TGAGAGAGCTGCTGCTATTCCTGAAGCTTGAAGAACTGCTCAAGAAAGCTCC 304  
 OY 392 TG 393  
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 DB 305 TG 306

RESULT 10  
 BD223239 446 bp DNA linear PAT 17-JUL-2003  
 LOCUS Method of genetic expression of polypeptide in plant.  
 DEFINITION BD223239  
 ACCESSION BD223239.1 GI:33033009  
 VERSION JP 2002523047-A/8.  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 other sequences; artificial sequences.  
 1 (bases 1 to 446)  
 Broekaert, W.F., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and Ray, J.A.  
 Ray, J.A.  
 Method of genetic expression of polypeptide in plant  
 Patent: JP 2002523047-A 8 30-JUL-2002;  
 SYNGENTA LTD  
 COMMENT  
 OS Artificial Sequence  
 PN JP 2002523047-A/8  
 PD 30-JUL-2002  
 PF 17-AUG-1999 JP 2000566429  
 PR 18-AUG-1998 GB 9818001.1 04-DEC-1998 GB 9826753.7 PI  
 WILLEM FRANS BROEKAERT, ISABELLE ELISA JEANNE  
 AUGUSTINE FRANCOIS,  
 PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI  
 ANTHONY RAY  
 PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P21/02//C12N5/10, PC  
 C12R1:91),  
 CC Description of Artificial Sequence: Synthetic sequence FH  
 Key Location/Qualifiers  
 FT CDS (3) .. (437).

## FEATURES

## source

1..446  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"

## ORIGIN

Query Match 38.6%; Score 172.2; DB 6; Length 446;  
 Best Local Similarity 93.3%; Pred. No. 7.3e-34;  
 Matches 180; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 155 AGATATGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAA 214  
 |||||  
 DB 65 AGATATGCATCCGTTAGTGGAGAACTATGCGAGAAAGCTAGCAAGACATGTCGGGAA 124  
 OY 215 CTGTGGCAATACGGGACATTTGTGACCAACCAATGTAATCATGGAGGGTGGCCCATGG 274  
 |||||

Db 125 CTGTGGCAACACGGGACATTGTGACACCAATGTAATCATGAGAGGTGGCGCTCACGG 184

Qy 275 AGCGTGCATGTGCGTAAACGGGAAACACATGTGTTCTGTACTTCAATTGTAAAGAC 334

Db 185 AGCGTGCATGTGCGTAAACGGGAAACACATGTGTTCTGTACTTCAATTGTAAAGAC 244

Qy 335 CGAAAAGCTTCT 347

Db 245 CGACGAGGTGCT 257

RESULT 11

LOCUS BD223244 1093 bp DNA linear PAT 17-JUL-2003

DEFINITION Method of genetic expression of polypeptide in plant.

ACCESSION BD223244

VERSION BD223244.1 GI:33033014

KEYWORDS JP 2002523047-A/13.

SOURCE JP 2002523047-A/13.

ORGANISM Synthetic construct

REFERENCE 1 (bases 1 to 1093)

AUTHORS Broekaert, W.F., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and Ray, J.A.

PI MUGEL, FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI ANTHONY RAY

PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P21/02// (C12N5/10, PC C12R1:91)

CC Description of genetic expression of polypeptide in plant

KEYWORDS Patent: JP 2002523047-A 13 30-JUL-2002;

COMMENT SINGENTA LTD

OS Artificial Sequence

PN JP 2002523047-A/13

PD 30-JUL-2002

PF 17-AUG-1999 JP 2000566429

PR 18-AUG-1998 GB 9818001.1, 04-DEC-1998 GB 9826753.7 PI

WILEM FRANS BROEKAERT, ISABELLE ELISA JEANNE AUGUSTINE FRANCOIS,

PI MUGEL, FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI ANTHONY RAY

PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P21/02// (C12N5/10, PC C12R1:91)

CC Description of Artificial Sequence: Synthetic sequence FH

KEYWORDS Location/Qualifiers

FT CDS Location/Qualifiers

FEATURES

source 1.1093

/organism="synthetic construct"

/mol\_type="genomic DNA"

/db\_xref="taxon:32630"

ORIGIN

Query Match 38.1%; Score 170; DB 6; Length 1093;

Best Local Similarity 84.3%; Pred. No. 2.8e-33;

Matches 204; Conservative 0; Mismatches 35; Indels 3; Gaps 1;

Qy 155 AGATATCGCATCGTGTAGAGAACTATGCGAGAACTAGCAAGACATGTCGGGAA 214

Db 65 AGATATCGCATCGTGTAGAGAACTATGCGAGAACTAGCAAGACATGTCGGGAA 124

Qy 215 CTGTGGCAATACGGGACATTGTGACCAACCAATGTAATCATGAGAGGTGGCGCCATGG 274

Db 125 CTGTGGCAATACGGGACATTGTGACCAACCAATGTAATCATGAGAGGTGGCGCCATGG 184

Qy 275 AGCGTGCATGTGCGTAAACGGGAAACACATGTGTTCTGTACTTCAATTGTAAAGAC 334

Db 185 AGCGTGCATGTGCGTAAACGGGAAACACATGTGTTCTGTACTTCAATTGTAAAGAC 244

Qy 335 CGAAAAGCTTCTCAAGCAAACTTAAG---CCGAAACATGCTCAAGCAAACTTA 391

Db 245 TGAGGAAGCTGCTGCTATTCCTGAAGCTTGAAGAACTTGTCTCAAGAAAGCTCC 304

Qy 392 TG 393

Db 305 TG 306

RESULT 12

LOCUS BD223233 522 bp DNA linear PAT 17-JUL-2003

DEFINITION Method of genetic expression of polypeptide in plant.

ACCESSION BD223233

VERSION BD223233.1 GI:33033003

KEYWORDS JP 2002523047-A/2.

SOURCE JP 2002523047-A/2.

ORGANISM Synthetic construct

REFERENCE 1 (bases 1 to 522)

AUTHORS Broekaert, W.F., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and Ray, J.A.

PI MUGEL, FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI ANTHONY RAY

PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P21/02// (C12N5/10, PC C12R1:91)

CC Description of genetic expression of polypeptide in plant

KEYWORDS Patent: JP 2002523047-A 2 30-JUL-2002;

COMMENT SINGENTA LTD

OS Artificial Sequence

PN JP 2002523047-A/2

PD 30-JUL-2002

PF 17-AUG-1999 JP 2000566429

PR 18-AUG-1998 GB 9818001.1, 04-DEC-1998 GB 9826753.7 PI

WILEM FRANS BROEKAERT, ISABELLE ELISA JEANNE AUGUSTINE FRANCOIS,

PI MUGEL, FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI ANTHONY RAY

PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P21/02// (C12N5/10, PC C12R1:91)

CC Description of Artificial Sequence: Synthetic sequence FH

KEYWORDS Location/Qualifiers

FT CDS Location/Qualifiers

FEATURES

source 1.522

/organism="synthetic construct"

/mol\_type="genomic DNA"

/db\_xref="taxon:32630"

ORIGIN

Query Match 37.9%; Score 169.2; DB 6; Length 522;

Best Local Similarity 95.6%; Pred. No. 4.4e-33;

Matches 174; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 155 AGATATCGCATCGTGTAGAGAACTATGCGAGAACTAGCAAGACATGTCGGGAA 214

Db 138 AGATATCGCATCGTGTAGAGAACTATGCGAGAACTAGCAAGACATGTCGGGAA 197

Qy 215 CTGTGGCAATACGGGACATTGTGACCAACCAATGTAATCATGAGAGGTGGCGCCATGG 274

Db 198 CTGTGGCAATACGGGACATTGTGACCAACCAATGTAATCATGAGAGGTGGCGCCATGG 257

Qy 275 AGCGTGCATGTGCGTAAACGGGAAACACATGTGTTCTGTACTTCAATTGTAAAGAC 334

Db 258 AGCGTGCATGTGCGTAAACGGGAAACACATGTGTTCTGTACTTCAATTGTCAAGC 317

Qy 335 CG 336

Db 318 TG 319

RESULT 13

LOCUS AX046745 460 bp DNA linear PAT 15-DEC-2000

DEFINITION Sequence 3 from Patent WO0068405.

ACCESSION AX046745

VERSION AX046745.1 GI:11876281

KEYWORDS

SOURCE Dimorphotheca sinuata (African daisy)

ORGANISM Dimorphotheca sinuata

Dimorphotheca sinuata

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Calenduleae; Dimorphotheca.



REFERENCE 1  
AUTHORS Miao, G.H., Weng, Z. and Famodu, O. O.  
TITLE Plant defensins  
JOURNAL Patent: WO 0068405-A 3 16-NOV-2000;  
E.I. DU PONT DE NEMOURS AND COMPANY (US)  
FEATURES  
SOURCE Location/Qualifiers  
1. .460  
/organism="Dimorphotheca sinuata"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:112408"  
ORIGIN  
Query Match 37.8%; Score 168.6; DB 6; Length 460;  
Best Local Similarity 81.6%; Pred. No. 6.3e-33;  
Matches 195; Conservative 0; Mismatches 44; Indels 0; Gaps 0;  
Qy 155 AGAATGCGATCCCTTGTGAGAACTATGGAAGAAAGTGAAGACATGTGGGAAA 214  
Db 87 AGAATGCGATCCCTTGTGAGAACTATGGAAGAAAGTGAAGACATGTGGGAAA 146  
Qy 215 CTGTGGCAATACGGGACATTTGACAAACCAATGTAATCATGGAGGGTGGCCCATGG 274  
Db 147 CTGTGGCAACACGGGACATTTGACAAACCAATGTAATCATGGAGGGTGGCCCATGG 206  
Qy 275 AGCGTGTATGTGGGTAAACGGAAACACATGTGTTCTGTACTTCAATTGTAAAAAGC 334  
Db 207 TGCCTGTATGTGGGTGGGAAACACATGTGTTCTGTACTTCAATTGTAAAAAGC 266  
Qy 335 CGAAAGCTTGCTCAAGCAAACTTAAAGCCGAACACTGCTCAAGCAAACTTAATG 393  
Db 267 CGAAAGCTTGCTCAAGCAAACTTAAAGCCGAACACTGCTCAAGCAAACTTAATG 325  
RESULT 14  
LOCUS AX046743 503 bp DNA linear PAT 15-DEC-2000  
DEFINITION Sequence 1 from Patent WO0068405.  
ACCESSION AX046743  
VERSION AX046743.1 GI:11876280  
KEYWORDS  
SOURCE Dimorphotheca sinuata (African daisy)  
ORGANISM Dimorphotheca sinuata  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; campanulids; Asterales; Asteroideae; Asteraceae;  
Calenduleae; Dimorphotheca.  
REFERENCE 1  
AUTHORS Miao, G.H., Weng, Z. and Famodu, O. O.  
TITLE Plant defensins  
JOURNAL Patent: WO 0068405-A 1 16-NOV-2000;  
E.I. DU PONT DE NEMOURS AND COMPANY (US)  
FEATURES  
SOURCE Location/Qualifiers  
1. .503  
/organism="Dimorphotheca sinuata"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:112408"  
ORIGIN  
Query Match 37.8%; Score 168.6; DB 6; Length 503;  
Best Local Similarity 81.6%; Pred. No. 6.3e-33;  
Matches 195; Conservative 0; Mismatches 44; Indels 0; Gaps 0;  
Qy 155 AGAATGCGATCCCTTGTGAGAACTATGGAAGAAAGTGAAGACATGTGGGAAA 214  
Db 80 AGAATGCGATCCCTTGTGAGAACTATGGAAGAAAGTGAAGACATGTGGGAAA 139

Qy 215 CTGTGGCAATACGGGACATTTGACAAACCAATGTAATCATGGAGGGTGGCCCATGG 274  
Db 140 CTGTGGCAACACGGGACATTTGACAAACCAATGTAATCATGGAGGGTGGCCCATGG 199  
Qy 275 AGCGTGTATGTGGGTAAACGGAAACACATGTGTTCTGTACTTCAATTGTAAAAAGC 334  
Db 200 TGCCTGTATGTGGGTGGGAAACACATGTGTTCTGTACTTCAATTGTAAAAAGC 259  
Qy 335 CGAAAGCTTGCTCAAGCAAACTTAAAGCCGAACACTGCTCAAGCAAACTTAATG 393  
Db 260 CGAAAGCTTGCTCAAGCAAACTTAAAGCCGAACACTGCTCAAGCAAACTTAATG 318

RESULT 15  
LOCUS BD223237 534 bp DNA linear PAT 17-JUL-2003  
DEFINITION Method of genetic expression of polypeptide in plant.  
ACCESSION BD223237  
VERSION BD223237.1 GI:33033007  
KEYWORDS JP 2002523047-A/6.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Broekaert, W.F., Francois, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and Ray, J.A.  
TITLE Method of genetic expression of polypeptide in plant  
JOURNAL Patent: JP 2002523047-A 6 30-JUL-2002;  
STINGENTA LTD  
OS Artificial Sequence  
PN JP 2002523047-A/6  
PD 30-JUL-2002  
PF 17-AUG-1998 JP 2000566429  
PR 18-AUG-1998 GB 9818001.1, 04-DEC-1998 GB 9826753.7 PI  
WILLEM FRANS BROEKAERT, ISABELLE ELSA JEANNE  
AUGUSTINE FRANCOIS,  
PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI  
ANTHONY RAY  
PC C12N15/09, A01H1/00, C07K1/12, C12N5/10, C12P21/02, C12N5/10, PC  
C12R1:91),  
PC C12N15/00, C12N5/00, C12N5/00, C12R1:91)  
CC Description of Artificial Sequence: Synthetic sequence FH  
Key Location/Qualifiers  
FT CDS Location/Qualifiers  
(76) . (525).  
FEATURES  
SOURCE Location/Qualifiers  
1. .534  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
ORIGIN

Query Match 37.5%; Score 167.2; DB 6; Length 534;  
Best Local Similarity 98.3%; Pred. No. 1.5e-32;  
Matches 169; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 155 AGAATGCGATCCCTTGTGAGAACTATGGAAGAAAGTGAAGACATGTGGGAAA 214  
Db 138 AGAATGCGATCCCTTGTGAGAACTATGGAAGAAAGTGAAGACATGTGGGAAA 197  
Qy 215 CTGTGGCAATACGGGACATTTGACAAACCAATGTAATCATGGAGGGTGGCCCATGG 274  
Db 198 CTGTGGCAACACGGGACATTTGACAAACCAATGTAATCATGGAGGGTGGCCCATGG 257  
Qy 275 AGCGTGTATGTGGGTAAACGGAAACACATGTGTTCTGTACTTCAATTGT 326  
Db 258 AGCGTGTATGTGGGTGGGAAACACATGTGTTCTGTACTTCAATTGT 309

Search completed: March 18, 2005, 14:31:02  
Job time : 2320 secs

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RESULT 2  
US-08-377-687-31  
Sequence 31, Application US/08377687  
Patent No. 5518525  
GENERAL INFORMATION:  
APPLICANT: BROEKERT, WILLEM F.  
APPLICANT: CAMMUE, BRUNO P.A.  
APPLICANT: OSBORN, RUPERT W.  
APPLICANT: REES, SARAH B.  
APPLICANT: TERRAS, FRANKY R.G.  
APPLICANT: VANDERLEYDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/377,687  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/002,480  
FILING DATE: 04-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-377-687-31

Query Match 22.3%; Score 99.4; DB 1; Length 150;  
Best Local Similarity 79.2%; Pred. No. 4.6e-21;  
Matches 118; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 177 GAACATGCGAAGAACTAGACAGCATGTCGGGAACTGTGCAATACGGGACATTGT 236  
DB 1 GACCTTGGAGAGAGGCTTCTAGACTTGTGGAACACGCGAAACACTGGACATTGC 60

QY 237 GACACCAATGTAAATCATGAGAGGTCGCGCCCATGAGCGTGTCAATGCGTAAACGGG 296  
DB 61 GATPACCAATGCAAGCTTGGAGGAGCTGCTCATGAGACTTGCATGTAAACGGA 120

QY 297 AAACACATGTGTTCTGTACTTCAATTG 325  
DB 121 AAGCATATGTGCTTCTGCTACTCACTG 149

*is there seq idb*

RESULT 3  
US-08-777-192-31  
Sequence 31, Application US/08777192  
Patent No. 5824869  
GENERAL INFORMATION:  
APPLICANT: BROEKERT, WILLEM F.

APPLICANT: CAMMUE, BRUNO P.A.  
APPLICANT: OSBORN, RUPERT W.  
APPLICANT: REES, SARAH B.  
APPLICANT: TERRAS, FRANKY R.G.  
APPLICANT: VANDERLEYDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/777,192  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/002,480  
FILING DATE: 04-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-777-192-31

Query Match 22.3%; Score 99.4; DB 1; Length 150;  
Best Local Similarity 79.2%; Pred. No. 4.6e-21;  
Matches 118; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 177 GAACATGCGAAGAACTAGACAGCATGTCGGGAACTGTGCAATACGGGACATTGT 236  
DB 1 GACCTTGGAGAGAGGCTTCTAGACTTGTGGAACACGCGAAACACTGGACATTGC 60

QY 237 GACACCAATGTAAATCATGAGAGGTCGCGCCCATGAGCGTGTCAATGCGTAAACGGG 296  
DB 61 GATPACCAATGCAAGCTTGGAGGAGCTGCTCATGAGACTTGCATGTAAACGGA 120

QY 297 AAACACATGTGTTCTGTACTTCAATTG 325  
DB 121 AAGCATATGTGCTTCTGCTACTCACTG 149

RESULT 4  
US-08-971-982-31  
Sequence 31, Application US/08971982  
Patent No. 6187904  
GENERAL INFORMATION:  
APPLICANT: BROEKERT, WILLEM F.  
APPLICANT: CAMMUE, BRUNO P.A.  
APPLICANT: OSBORN, RUPERT W.  
APPLICANT: REES, SARAH B.  
APPLICANT: TERRAS, FRANKY R.G.  
APPLICANT: VANDERLEYDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/971,982  
FILING DATE: 17-No. 6187904-1597  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/002,480  
FILING DATE: 04-JAN-1993

ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944

INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear

MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-08-971-982-31

Query Match 22.3%; Score 99.4; DB 3; Length 150;  
Best Local Similarity 79.2%; Pred. No. 4,66-21;  
Matches 118; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 177 GAACATGCGAGAAAGCTAGCAAGACATGTCGGGAAAGCTGGCAATAGCGGCAATTGT 236  
DB 1 GAGCTTTGCGAGAAAGCTTTAGACTTGTCTGAAAGCTGGGAAACATGCGACATTGC 60

QY 237 GACACCAATGTAATCATGAGGAGGTCGCCCATGAGCGTGTCTATGTCGTAACGGG 296  
DB 61 GATACCAATGCAAGCTCTGGGAGGAGCTGCTCATGAGCTTCCATGTTAGAAACGA 120

QY 297 AACACATGTTCTTCTGTACTTCAATTG 325  
DB 121 AAGCATATGCTTCTGTACTTCAACTG 149

RESULT 5  
US-08-377-687-33  
Sequence 33, Application US/08377687  
Patent No. 5538525

GENERAL INFORMATION:  
APPLICANT: BROEKERT, WILLEM F.  
APPLICANT: CAMMUE, BRUNO P.A.  
APPLICANT: OSBORN, RUPERT W.  
APPLICANT: REES, SARAH B.  
APPLICANT: TERRAS, FRANKY R.G.  
APPLICANT: VANDERLEIDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/377,687  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/002,480  
FILING DATE: 04-JAN-1993

ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944

INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear

MOLECULE TYPE: cDNA  
US-08-377-687-33

Query Match 20.5%; Score 91.4; DB 1; Length 150;  
Best Local Similarity 75.8%; Pred. No. 1,46-18;  
Matches 113; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 177 GAACATGCGAGAAAGCTAGCAAGACATGTCGGGAAAGCTGGCAATAGCGGCAATTGT 236  
DB 1 GAGCTTTGCGAGAAAGCTTTAGACTTGTCTGAAAGCTGGGAAACATGCGACATTGC 60

QY 237 GACACCAATGTAATCATGAGGAGGTCGCCCATGAGCGTGTCTATGTCGTAACGGG 296  
DB 61 GATACCAATGCAAGCTCTGGGAGGAGCTGCTCATGAGCTTCCATGTTAGAAACGA 120

QY 297 AACACATGTTCTTCTGTACTTCAATTG 325  
DB 121 AAGCATATGCTTCTGTACTTCAACTG 149

RESULT 6  
US-08-777-192-33  
Sequence 33, Application US/08777192  
Patent No. 5824869

GENERAL INFORMATION:  
APPLICANT: BROEKERT, WILLEM F.  
APPLICANT: CAMMUE, BRUNO P.A.  
APPLICANT: OSBORN, RUPERT W.  
APPLICANT: REES, SARAH B.  
APPLICANT: TERRAS, FRANKY R.G.  
APPLICANT: VANDERLEIDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/777,192  
FILING DATE:  
CLASSIFICATION:

not instant  
SEA ID 6

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/002,480  
FILING DATE: 04-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-777-192-33

Query Match 20.5%; Score 91.4; DB 1; Length 150;  
Best Local Similarity 75.8%; Pred. No. 1,4e-18;  
Matches 113; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 177 GAACATGCGAGAAAGCTAGACAGATGTCGGGAAACTGTGGCAATAGCGGACATTGT 236  
DB 1 GAGCTTGGCAGAAAGCTTCTTAAGACTTGTCTGGAACTGCGAAACACTAAGCATTGC 60  
QY 237 GACAACCAATGTAATCATGAGGAGGTGCGGCCCATGAGCCGTGTGTCGTTAACGGG 236  
DB 61 GATGATCAATGCAAGCTTGGGAGGAGCTGCTCATGAGCTTGCATGTGTAAGAAACGGA 120  
QY 297 AACACATGTTCTTCTGTACTTCAATTG 325  
DB 121 AAGCATATGCTTCTGTACTTCAACTG 149

RESULT 7  
US-08-971-982-33  
Sequence 33, Application US/08971982  
Patent No. 6187904  
GENERAL INFORMATION:  
APPLICANT: BROEKAERT, WILLEM F.  
CAMMUE, BRUNO P.A.  
OSBORN, RUPERT W.  
REES, SARAH B.  
TERRAS, FRANKY R.G.  
VANDERLEYDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DABRY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/971,982  
FILING DATE: 17-NO. 6187904-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/002,480  
FILING DATE: 04-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-08-971-982-33

Query Match 20.5%; Score 91.4; DB 3; Length 150;  
Best Local Similarity 75.8%; Pred. No. 1,4e-18;  
Matches 113; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 177 GAACATGCGAGAAAGCTAGACAGATGTCGGGAAACTGTGGCAATAGCGGACATTGT 236  
DB 1 GAGCTTGGCAGAAAGCTTCTTAAGACTTGTCTGGAACTGCGAAACACTAAGCATTGC 60  
QY 237 GACAACCAATGTAATCATGAGGAGGTGCGGCCCATGAGCCGTGTGTCGTTAACGGG 236  
DB 61 GATGATCAATGCAAGCTTGGGAGGAGCTGCTCATGAGCTTGCATGTGTAAGAAACGGA 120  
QY 297 AACACATGTTCTTCTGTACTTCAATTG 325  
DB 121 AAGCATATGCTTCTGTACTTCAACTG 149

RESULT 8  
US-08-377-687-34  
Sequence 34, Application US/08377687  
Patent No. 5538525  
GENERAL INFORMATION:  
APPLICANT: BROEKAERT, WILLEM F.  
CAMMUE, BRUNO P.A.  
OSBORN, RUPERT W.  
REES, SARAH B.  
TERRAS, FRANKY R.G.  
VANDERLEYDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DABRY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/377,687  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/002,480  
FILING DATE: 04-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both

TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-377-687-34

Query Match 19.4%; Score 86.6; DB 1; Length 150;  
Best Local Similarity 73.8%; Pred. No. 4.3e-17;  
Matches 110; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 177 GAACATGCGAGAAAGCTAGACATGTCGGGAAACTGTGGCAATACGGACATTGT 236  
DB 1 GAGCTTTCGAGAAAGGCTTCTTAAGACTTGGTCTGGAACACTGCGAAACACTAAGCATTGC 60  
QY 237 GACACCAATGTAATATCATGAGAGGTCGGCCCATGAGCGTGTCAATGCGTAACGGG 296  
DB 61 GATTAACAAGTCAAGTCTTGGAGAGGAGCTGCTCATGAGCTTGCATGTTAGATCTTGA 120  
QY 297 AAACACATGTTCTTCTGTTACTTCAATG 325  
DB 121 AAGCATATGCTTCTCTGCTACTTCAATG 149

## RESULT 9

US-08-777-192-34  
Sequence 34, Application US/08777192  
Patent No. 5824869  
GENERAL INFORMATION:  
APPLICANT: BROEKAERT, WILLEM F.  
APPLICANT: CAMMUE, BRUNO P.A.  
APPLICANT: OSBORN, RUPERT W.  
APPLICANT: REES, SARAH B.  
APPLICANT: TERRAS, FRANKY R.G.  
APPLICANT: VANDERLEIDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DAREY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/777,192  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/002,480  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-777-192-34

Query Match 19.4%; Score 86.6; DB 1; Length 150;  
Best Local Similarity 73.8%; Pred. No. 4.3e-17;  
Matches 110; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 177 GAACATGCGAGAAAGCTAGACATGTCGGGAAACTGTGGCAATACGGACATTGT 236  
DB 1 GAGCTTTCGAGAAAGGCTTCTTAAGACTTGGTCTGGAACACTGCGAAACACTAAGCATTGC 60  
QY 237 GACACCAATGTAATATCATGAGAGGTCGGCCCATGAGCGTGTCAATGCGTAACGGG 296  
DB 61 GATTAACAAGTCAAGTCTTGGAGAGGAGCTGCTCATGAGCTTGCATGTTAGATCTTGA 120  
QY 297 AAACACATGTTCTTCTGTTACTTCAATG 325  
DB 121 AAGCATATGCTTCTCTGCTACTTCAATG 149

## RESULT 10

US-08-971-982-34  
Sequence 34, Application US/08971982  
Patent No. 6187904  
GENERAL INFORMATION:  
APPLICANT: BROEKAERT, WILLEM F.  
APPLICANT: CAMMUE, BRUNO P.A.  
APPLICANT: OSBORN, RUPERT W.  
APPLICANT: REES, SARAH B.  
APPLICANT: TERRAS, FRANKY R.G.  
APPLICANT: VANDERLEIDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DAREY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/971,982  
FILING DATE: 17-NO. 6187904-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/002,480  
FILING DATE: 04-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 150 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 34:  
US-08-971-982-34

Query Match 19.4%; Score 86.6; DB 3; Length 150;  
Best Local Similarity 73.8%; Pred. No. 4.3e-17;  
Matches 110; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 177 GAACATGCGAGAAAGCTAGACATGTCGGGAAACTGTGGCAATACGGACATTGT 236  
DB 1 GAGCTTTCGAGAAAGGCTTCTTAAGACTTGGTCTGGAACACTGCGAAACACTAAGCATTGC 60  
QY 237 GACACCAATGTAATATCATGAGAGGTCGGCCCATGAGCGTGTCAATGCGTAACGGG 296  
DB 61 GATTAACAAGTCAAGTCTTGGAGAGGAGCTGCTCATGAGCTTGCATGTTAGATCTTGA 120

QY 297 AACACATGCTTCTGTTACTTCAATTG 325  
Db 121 AACGATATGCTTCTGTTACTTCAACTG 149

## RESULT 11

US-08-377-687-36  
Sequence 36, Application US/08377687  
Patent No. 5538525  
GENERAL INFORMATION:  
APPLICANT: BROEKAERT, WILLEM F.  
APPLICANT: CAMMUE, BRUNO P.A.  
APPLICANT: OSBORN, RUPERT W.  
APPLICANT: REES, SARAH B.  
APPLICANT: TERRAS, FRANKY R.G.  
APPLICANT: VANDERLEIDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/377,687  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/002,480  
FILING DATE: 04-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 147 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-377-687-36

Query Match 13.1%; Score 58.4; DB 1; Length 147;  
Best Local Similarity 66.9%; Pred. No. 2.5e-08;  
Matches 99; Conservative 0; Mismatches 46; Indels 3; Gaps 1;  
QY 178 AACTATCGAGAAAGCTAGCAAGCATGTGGGAAACTGTGCAATACGGGACATTGTG 237  
Db 2 ACCTTGCGAGAGAGCTTCTTACTTGACTGAACTGGAACTGGGAAACACTGGACATTGCG 61  
QY 238 ACAACCAATGTAATCATGGAGAGGTGCGCCCATGAGCGTGTCAATGTGCTTAACGGGA 297  
Db 62 ATACTCAATGCAAGAACTGGAGAGTCTGTAAGCATGAGGCTTGCCATTAAG---AGAGGAA 118  
QY 298 AACCATGTGTTTCTGTTACTTCAATTG 325  
Db 119 ACTGGAAGTCTTCTGTTACTTCAATTG 146

RESULT 12  
US-08-777-192-36

Sequence 36, Application US/08777192  
Patent No. 5824869  
GENERAL INFORMATION:  
APPLICANT: BROEKAERT, WILLEM F.  
APPLICANT: CAMMUE, BRUNO P.A.  
APPLICANT: OSBORN, RUPERT W.  
APPLICANT: REES, SARAH B.  
APPLICANT: TERRAS, FRANKY R.G.  
APPLICANT: VANDERLEIDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/777,192  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/002,480  
FILING DATE: 04-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 147 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-777-192-36

Query Match 13.1%; Score 58.4; DB 1; Length 147;  
Best Local Similarity 66.9%; Pred. No. 2.5e-08;  
Matches 99; Conservative 0; Mismatches 46; Indels 3; Gaps 1;  
QY 178 AACTATCGAGAAAGCTAGCAAGCATGTGGGAAACTGTGCAATACGGGACATTGTG 237  
Db 2 ACCTTGCGAGAGAGCTTCTTACTTGACTGAACTGGGAAACACTGGACATTGCG 61  
QY 238 ACAACCAATGTAATCATGGAGAGGTGCGCCCATGAGCGTGTCAATGTGCTTAACGGGA 297  
Db 62 ATACTCAATGCAAGAACTGGAGAGTCTGTAAGCATGAGGCTTGCCATTAAG---AGAGGAA 118  
QY 298 AACCATGTGTTTCTGTTACTTCAATTG 325  
Db 119 ACTGGAAGTCTTCTGTTACTTCAATTG 146

RESULT 13  
US-08-971-982-36  
Sequence 36, Application US/08971982  
Patent No. 6187904  
GENERAL INFORMATION:  
APPLICANT: BROEKAERT, WILLEM F.  
APPLICANT: CAMMUE, BRUNO P.A.  
APPLICANT: OSBORN, RUPERT W.  
APPLICANT: REES, SARAH B.  
APPLICANT: TERRAS, FRANKY R.G.



VANDERLEYDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: CUSHMAN DABRY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/971,982  
FILING DATE: 17-NO. 6187904-1997  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/002,480  
FILING DATE: 04-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 147 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
US-08-971-982-36  
Query Match 13.1%; Score 58.4; DB 3; Length 147;  
Best Local Similarity 66.9%; Pred. No. 2.5e-08;  
Matches 99; Conservative 0; Mismatches 46; Indels 3; Gaps 1;  
Qy 178 AACTATGGAGAAAGCTAGCAAGCATGTCGGGAACTGTGCAATACGAGCATTTGTG 237  
Db 2 ACCTTGGAGAGAGCTTCTTACTTGACTGGAACTGGGAACTGGACATTGCG 61  
Qy 238 ACAACCAATGTAATTCATGGAGGGTGGCCCATGAGCGTGTCTATGTCGTTAACGGGA 297  
Db 62 ATACTCAATGAGAAAGCTGGAGTCTGTGAAGCATGAGGCTTGCATTAAG---AGAGGA 118  
Qy 298 AACCATGTCTTCTGTTACTTCAATTG 325  
Db 119 ACTGGAAGTCTTCTGCTACTTGCATTG 146  
RESULT 14  
US-08-627-706-14  
Sequence 14, Application US/08627706  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip M.  
APPLICANT: Wu, Yonnie S.  
APPLICANT: Rosenberger, Cindy A.  
TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Charles E. Cohen, Monsanto Company, BBAF  
STREET: 700 Chesterfield Village Parkway No. 5773696th  
CITY: St. Louis  
STATE: Missouri

COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/627,706  
FILING DATE:  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: Cohen, Charles E.  
REGISTRATION NUMBER: 34,565  
REFERENCE/DOCKET NUMBER: 38-21 (10700)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)537-6224  
TELEFAX: (314)537-6047  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 270 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-627-706-14  
Query Match 10.0%; Score 44.6; DB 1; Length 270;  
Best Local Similarity 53.8%; Pred. No. 0.00065;  
Matches 92; Conservative 0; Mismatches 79; Indels 0; Gaps 0;  
Qy 163 CATCCGTTAGTGAGACTAGTACGAGAAAGTACAGACATGTCGGGAACTGTGCA 222  
Db 95 CAATGTGATGACAGAGTTGTGTCAGAGACCAAGTGGACATGTCAGAGCTTTGTGGA 154  
Qy 223 ATACGGACATGTGTGACACCAATGTAAATCAGGAGGGTGGCCCATGAGACGTTGC 282  
Db 155 ACAACATGATGACGAGGAGCAACCAATGCAAAACCTTGAAGGACAGAACAGGATCTTGA 214  
Qy 283 ATGCGCTAACGGGAAACACATGCTTCTTACTTCAATTTGTAATAAAG 333  
Db 215 ACTATGTTCTCCAGCTCAGTCAAAATGTAATTTGTTACTTCCATGTTAATAAG 265  
RESULT 15  
US-09-103-489-14  
Sequence 14, Application US/09103489  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip M.  
APPLICANT: Wu, Yonnie S.  
APPLICANT: Rosenberger, Cindy A.  
TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Charles E. Cohen, Monsanto Company, BBAF  
STREET: 700 Chesterfield Village Parkway No. 6215048th  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/103,489  
FILING DATE: 24-JUN-1998  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:

NAME: Cohen, Charles E.  
REGISTRATION NUMBER: 34,565  
REFERENCE/DOCKET NUMBER: 38-21 (10700)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 537-6224  
TELEFAX: (314) 537-6047  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 270 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-09-103-489-14

Query Match 10.0%; Score 44.6; DB 3; Length 270;  
Best Local Similarity 53.8%; Pred. No. 0.00065;  
Matches 92; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 163 CATCGTTAGTGAGAACTATGCGAGAAAGCTAGCAAGCATGTGCGGAAACTGTGGCA 222  
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Db 95 CAATGTGTGATGCAAGTTGTGCGAGAGACCAAGTGGGACATGGTCAGAGTTGTGGGA 154  
QY 223 ATAGGGGACATGTGTGAGAACCAATGTAATCATGGGAGGTCGCCCATGGAGCGTTC 282  
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Db 155 ACAACAATGATGAGAGAACCAATGAGAAACCTTGAAAGAGCAACACGATCTTGCA 214  
QY 283 ATGTGCGTAAAGGAGAAACACATGTGTTCTGTACTTCAATGTGTAATAAG 333  
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Db 215 ACTATGTCTTCCAGCTCACAAATGTATTTGTTACTTCCCATGTTAATAAG 265

Search completed: March 18, 2005, 16:31:56  
Job time : 137 secs